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OM nucleic - nucleic search, using sw model

Run on: December 29, 2004, 13:38:09 ; Search time 2260 Seconds
(without alignments)
9353.317 Million cell updates/sec

Title: US-09-851-138c-51

Perfect score: 447
Sequence: 1 gagcgaaatatttcgcaac.....aggactgcacgttccatc 447

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hg: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sb: 12: gb_sy: 13: gb_un: 14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445.8	99.7	447	6 A50396	A50396 Sequence 51
2	445.8	99.7	447	6 AR127536	AR127536 Sequence 51
3	445.8	99.7	447	14 HPCCORREAL	L39317 Hepatitis C
4	445.8	99.7	447	14 HPCCK049A5	D49749 Hepatitis C
5	393	87.9	1584	14 HPCCK055A6	D49750 Hepatitis C
6	393	87.9	1584	14 HPCCK070A8	D49752 Hepatitis C
7	393	87.9	1584	14 HPCCK049R1	D49747 Hepatitis C
8	389.8	87.2	1584	14 HPCCK030A3	D49745 Hepatitis C
9	388.2	86.8	1584	14 HPCCK072A9	D49753 Hepatitis C
10	388.2	86.8	1584	14 HPCCK072A9	D49753 Hepatitis C
11	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C
12	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C
13	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C
14	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C
15	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C
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17	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C
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19	355.8	87.2	1505	14 HPCCK0125C	D16614 Hepatitis C

20	236.2	52.8	541	6 A40617	A40617 Sequence 17
21	236.2	52.8	541	6 AX031591	AX031591 Sequence
22	236.2	52.8	541	6 AX031595	AX031595 Sequence
23	236.2	52.8	541	6 AX031861	AX031861 Sequence
24	236.2	52.8	541	6 AX031865	AX031865 Sequence
25	236.2	52.8	541	6 AX032131	AX032131 Sequence
26	236.2	52.8	541	6 AX032135	AX032135 Sequence
27	236.2	52.8	541	6 BD172130	BD172130 New seq
28	236.2	52.8	541	6 BD172132	BD172132 New seq
29	236.2	52.8	541	6 HPCCORREH	D16603 Hepatitis C
30	236.2	52.8	541	6 HPCSTRUTC	L12355 Hepatitis C
31	234.6	52.5	541	6 A40619	A40619 Sequence 19
32	234.6	52.5	541	6 AX031597	AX031597 Sequence
33	234.6	52.5	541	6 AX031867	AX031867 Sequence
34	234.6	52.5	541	6 AX032137	AX032137 Sequence
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37	234.6	52.5	9456	14 HPCCK0125C	D1763 Hepatitis C
38	233	52.1	541	6 A40615	A40615 Sequence 15
39	233	52.1	541	6 A40621	A40621 Sequence 21
40	233	52.1	541	6 A40625	A40625 Sequence 25
41	233	52.1	541	6 A40627	A40627 Sequence 27
42	233	52.1	541	6 AX031593	AX031593 Sequence
43	233	52.1	541	6 AX031599	AX031599 Sequence
44	233	52.1	541	6 AX031603	AX031603 Sequence
45	233	52.1	541	6 AX031605	AX031605 Sequence

ALIGNMENTS

RESULT 1	A50396	Sequence 51 from Patent WO9613590.	447 bp	DNA	linear	PAT 07-MAR-1997
LOCUS	A50396					
DEFINITION	A50396					
ACCESSION	A50396					
VERSION	A50396.1	GI:2303407				
KEYWORDS	unclassified					
SOURCE	unclassified					
ORGANISM	unclassified					
REFERENCE	1 (bases 1 to 447)					
AUTHORS	Maertens G. and Stuyver L.					
TITLE	NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS					
JOURNAL	PATENT: WO 9613590-A 51 09-MAY-1996;					
COMMENT	INNOGENETICS NV. (BE)					
FEATURES	Other publication AU 3844095 960523.					
source	Location/Qualifiers					
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Matches 447;	Conservative 0;	Mismatches 0;				
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DB	1	GACGGAATTAATTCGCAACAGGAAATTACCGTGTCTCTTCTCTATCTCTCTG	60			
QY	61	GCTTGTCTCTACGCTGCTTACACCCACAGCGGAGTGAAGTACCGTAATGCTTCGGA	120			
DB	61	GCTTGTCTCTACGCTGCTTACACCCACAGCGGAGTGAAGTACCGTAATGCTTCGGA	120			
QY	121	CTCTACATGTAATTAATTCGCAACAGGAAATTACCGTGTCTCTTCTCTATCTCTG	180			
DB	121	CTCTACATGTAATTAATTCGCAACAGGAAATTACCGTGTCTCTTCTCTATCTCTG	180			
QY	181	ATCCCTCACTTACCTGCTGTCTCCCTGCTACCGTGTGCAATCATCAAGATCTCG	240			
DB	181	ATCCCTCACTTACCTGCTGTCTCCCTGCTACCGTGTGCAATCATCAAGATCTCG	240			

Dd		181	ATCTCCACCTTAACCTGGCGCTGTGTCCTCCCTGCAGTACGCTCTGGCAATAATCATGAAGTCTGG	240
Oy		241	ATCCCTGTGAGGCCCYAACCGCTGCGCGGTGAAGTGCCCTGCGCCGCCACCCTCTCTCCGC	300
Dd		241	ATCCCTGTGAGGCCCYAACCGCTGCGCGGTGAAGTGCCCTGCGCCGCCACCCTCTCTCCGC	300
Oy		301	ACGCACGTGAGATATATATGTGTGGGRRCCGGCACCTTAATGTCTCAGCTCTCTTAGGTAGAAGAC	360
Dd		301	ACGCACGTGAGATATATATGTGTGGGRRCCGGCACCTTAATGTCTCAGCTCTCTTAGGTAGAAGAC	360
Oy		361	CTTTGTGAGAGCGCTATTCTTGTGTGGGAGAGGGGTTCTGATGGAGACATCGCCAGATTGG	420
Dd		361	CTTTGTGAGAGCGCTATTCTTGTGTGGGAGAGGGGTTCTGATGGAGACATCGCCAGATTGG	420
Oy		421	ACTGTCCAGAGACTGCACCTGTTCCATC	447
Dd		421	ACTGTCCAGAGACTGCACCTGTTCCATC	447
RESULT 2				
LOCUS	AR127536	447 bp	DNA	linear
DEFINITION	Sequence 51 from patent US 6180768.			PAT 16-MAY-2001
ACCESSION	AR127536			
VERSION	AR127536.1	GI:14114131		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	Maertens,G. and Stuyver,L.			
TITLE	Sequences of hepatitis C virus genotypes and their use as prophylactic, therapeutic and diagnostic agents			
JOURNAL FEATURES	Patent: US 6180768-A 51.30-JAN-2001;			
source	location/Qualifiers 1..447 /organism="unknown" /mol_type="unassigned DNA"			
ORIGIN				
Query Match	99.7%; Score 445.8; DB 6; Length 447;			
Beet Local Similarity	100.0%; Fred. No. 9.5e-109;			
Matches	447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy		1	GACGGAAATTAATTTTCGCAACAGGGAATTTAACCCTGGTGTCTCTTATCTTCTCTCG	60
Dd		1	GACGGAAATTAATTTTCGCAACAGGGAATTTAACCCTGGTGTCTCTTATCTTCTCTCG	60
Oy		61	GCTTGTTCCTCAVCGCTGCTTACACCCAAGCCGGGCTGAGTACCGTAATGCTCCGGA	120
Dd		61	GCTTGTTCCTCAVCGCTGCTTACACCCAAGCCGGGCTGAGTACCGTAATGCTCCGGA	120
Oy		121	CTTATCATGTGAATCTAACAAGACTGCAAGTAAACGTTACTATCTGTATGAGAGCCGGGATATT	180
Dd		121	CTTATCATGTGAATCTAACAAGACTGCAAGTAAACGTTACTATCTGTATGAGAGCCGGGATATT	180
Oy		181	ATCTCCACTTAACCTGGCTGTGTCCCTGCGGTAAGCTCTGGCAATATCAAGATCTGG	240
Dd		181	ATCTCCACTTAACCTGGCTGTGTGTCCCTGCGGTAAGCTCTGGCAATATCAAGATCTGG	240
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Dd		241	ATCCCTGTGAGCCCYAACCGCTGCGCGGTGAAGTGCCCTGCGCCGCCACCCTCTCTCCGC	300
Oy		301	ACGCACGTGAGATATATGTGTGGGRRCCGGCACCTTAATGTCTCAGCTCTCTTAGGTAGAAGAC	360
Dd		301	ACGCACGTGAGATATATGTGTGGGRRCCGGCACCTTAATGTCTCAGCTCTCTTAGGTAGAAGAC	360
Oy		361	CTTTGTGAGAGCGCTATTCTTGTGTGGGAGAGGGGTTCTGATGGAGACATCGCCAGATTGG	420
Dd		361	CTTTGTGAGAGCGCTATTCTTGTGTGGGAGAGGGGTTCTGATGGAGACATCGCCAGATTGG	420
Oy		421	ACTGTCCAGAGACTGCACCTGTTCCATC	447

Db		421	ACTGTCCAGGACCTGCACACTGTTTCATC	447	
RESULT 3	HPCOREBEAL			447 bp ss-RNA	linear VRL 16-OCT-2001
DEFINITION	Hepatitis C virus type 3 clone NL96 precursor protein gene, partial cde.				
ACCESSION	L39317				
VERSION	L39317.1			GI:845497	
SOURCE	Hepatitis C virus type 3				
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.				
REFERENCE	1 (bases 1 to 447)				
AUTHORS	van Doorn,L.J., Kleter,B., Stuyver,L., Maertens,G., Brouwer,H., Schalm,S., Helfink,R. and Quint,W.				
TITLE	Analysis of hepatitis C virus genotypes by a line probe assay and correlation with antibody profiles				
JOURNAL	J. Hepatol. 21 (1), 122-129 (1994)				
MEDLINE	95052487				
PUBMED	7525693				
REFERENCE	2 (bases 1 to 447)				
AUTHORS	van Doorn,L.J., Kleter,B., Stuyver,L., Maertens,G., Brouwer,J.T., Schalm,S.W., Helfink,R.A. and Quint,W.G.				
TITLE	Sequence analysis of hepatitis C virus genotypes 1 to 5 reveals multiple novel subtypes in the Benelux countries				
JOURNAL	J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995)				
MEDLINE	97201609				
PUBMED	9049395				
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Dd	1 GACGGAAATTATTTGCGAACAGGGAATTTCCTGGTCTCTTCTCTATCTTCTCTCG	60			
Oy	61 GCTTGTTCTCATGCTTGCCTTAACACCACAGCCGGGCTGAGATACCGTAATGCTCCGGA	120			
Dd	61 GCTTGTTCTCATGCTTGCCTTAACACCACAGCCGGGCTGAGATACCGTAATGCTCCGGA	120			
Oy	121 CTTCACATGGTAATACTAACAAGTAGATATGATATGAGGCCGGGGAATATT	180			
Dd	121 CTTCACATGGTAATACTAACAAGTAGATATGATATGAGGCCGGGGAATATT	180			
Oy	181 ATCTCCACTTACCTGGCTGTGTCCTCTGGCTACGCTCTGGCAATACATCAAGATGCTGG	240			
Dd	181 ATCTCCACTTACCTGGCTGTGTCCTCTGGCTACGCTCTGGCAATACATCAAGATGCTGG	240			

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OY		301	ACGACAGTGATATGATGATGGTGGGGRCGGCGCACCCATTATGCTCAGCTCTTACGTAGAGAAC	360
Df		301	ACGACAGTGATATGATGATGGTGGGGRCGGCGCACCCATTATGCTCAGCTCTTACGTAGAGAAC	360
OY		361	CTTTGTGAGAGGCTATTTCTTGTGTGGCGAAGGGGTTCTATGAGACATCGCCAGCATTTGG	420
Df		361	CTTTGTGAGAGGCTATTTCTTGTGTGGCGAAGGGGTTCTATGAGACATCGCCAGCATTTGG	420
OY		421	ACTGTCAGAGACTGCACATGTTCCATC	447
Df		421	ACTGTCAGAGACTGCACATGTTCCATC	447
RESULT 4				
HPCJKO49AS				
LOCUS		1584 bp	RNA	linear VRL 10-FEB-1999
DEFINITION		Hepatitis C virus isolate JK049 gene for core, env, and part of E2/NS1, partial cds.		
ACCESSION		D49749.1	GI:1197110	
VERSION		D49749.1	GI:1197110	
KEYWORDS		core, env, and part of E2/NS1.		
SOURCE		Hepatitis C virus		
ORGANISM		Hepatitis C virus		
REFERENCE		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.		
AUTHORS		1 (stees)		
TITLE		Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tenda,F., Isemane,L.A., Miyakawa,Y. and Mayumi,M. Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups		
JOURNAL		U. Gen. Virol. 77 (Pt 2), 293-301 (1996)		
MEDLINE		96226020		
PUBMED		8627233		
REFERENCE		2 (bases 1 to 1584)		
AUTHORS		Okamoto,H.		
JOURNAL		Unpublished		
REFERENCE		3 (bases 1 to 1584)		
TITLE		Okamoto,H.		
JOURNAL		Direct Submission		
REFERENCE		Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School, Immunology Division; Minami Kawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail: hokamoto@jichi.ac.jp) Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)		
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CDS				
5'UTR				

ORIGIN	ASGAFTTSLFSTGCAKOPHLVNV"
Query Match	87.9%; Score 393; DB 14; Length 1584;
Beet Local Similarity	91.9%; Pred. No. 1.5e-94;
Matches 411; Conservative	3; Mismatches 33; Indels 0; Gaps 0;
Qy	1 GACGAGATTAATTTCGACAGAGGAATTACACCTGCTCTTCTCTATCTTCTCTG 60
Db	817 GACGAGATTAATTTCGACAGAGGAATTACCTGCTCTTCTCTATCTTCTCTG 876
Qy	61 GCTTTGTTTCATGCTTGTCTTACACCCACAGCCGGCGTGAATACCGTAATGCTCCGGA 120
Db	877 GCTTTGCTTCATGCTTGTCTTACACCCACAGCCGGCGTGAATACCGTAATGCTCCGGA 936
Qy	121 CTCTACATGTAATACGACTGAGTAAGGTAATGTAATGTAATGAGGCGCGGAGATATT 180
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Qy	181 ATCTTCACATTAACCTGAGCTGTGTCTCCCTGCGTAAGCTCTGGAATACATCAAGATGCTG 240
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Db	1177 CTTTGTGAGCGCTATTCTTGTGGGACGAGGTTCTCATATGAGACATTCGACGATTGG 1236
Qy	421 ACTGTCCAGGACGCACTGTTCATC 447
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RESULT 5	
HPCUK055A6	1584 bp RNA linear VRL 10-FEB-1999
LOCUS	
DEFINITION	Hepatitis C virus isolate UK05 gene for core, env, and part of
ACCESSION	E2/NSI, partial cds.
VERSION	D49750.1
KEYWORDS	D49750.1 GI:1197114
SOURCE	core, env, and part of E2/NSI.
ORGANISM	Hepatitis C virus
REFERENCE	Hepatitis C virus
AUTHORS	Vinuesa; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
TITLE	1 (sites)
JOURNAL	Tohite, H., Okamoto, H., Itakura, H., Kishimoto, J., Tsuda, F.,
MEDLINE	Lemana, L.A., Miyakawa, Y. and Mayumi, M.
PUBMED	Hepatitis C virus variants from Jakarta, Indonesia classifiable
REFERENCE	into novel genotypes in the second (2e and 2f), tenth (10a) and
AUTHORS	eleventh (11a) genetic groups
JOURNAL	J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
TITLE	96226020
REFERENCE	2 (bases 1 to 1584)
AUTHORS	Okamoto, H.
JOURNAL	Unpublished
TITLE	3 (bases 1 to 1584)
JOURNAL	Okamoto, H.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
REFERENCE	Immunology Division, Minamikawachi-machi, Kawachi-gun, Tochigi
AUTHORS	329-04, Japan (E-mail: hokamoto@jichi.ac.jp).
TITLE	Tel: 0285-44-2111 (ex. 3334), Fax: 0285-44-1557)
FEATURES	Location/Qualifiers
SOURCE	1..1584

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ORIGIN

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Query Match      87.9%; Score 393; DB 14; Length 1584;
Best Local Similarity 91.9%; Pred. No. 1.5e-94;
Matches 411; Conservative 3; Mismatches 33; Indels 0; Gaps 0;
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QY	1	GACGGAATTAATTTTCGAAACAGGGAAATTACCTGGTTCCTTTCTCTATCTTCCTCTCG	60
Db	817	GACGGAATCAATTTTCGACACAGGGAATTTACTGGTTCCTTTCTCTATCTTTCTCTG	876
QY	61	GCTTGTGTTTCATGCTGTTGCTTACACCCACAGCCGGGCTGAGTACCGTAAATGCTCCGGA	120
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QY	181	ATCTCCACTTACCTGAGCTGTGTCCCTGCAGTACGCTTGACAAATACATCAAGAATGCTGG	240
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Db	1117	ACGCAACGTGAATGATGATGGGAGGCCGACACCCGTATCTCAGCTCTTAAAGTGGGAAT	1176
QY	361	CTTTGTGAGAGGCTAATTTCTTGTGGGAGAGGGTTCTCATGAGAATCGCCAGCATTTGG	420
Db	1177	CTTTGTGAGAGGCTGTGTTCTTGTGGGAGAGGGTTCTCATGAGAATCGCCAGCATTTGG	1236
QY	421	ACTGTCCAGGACTGCAACTGTTCATC 447	
Db	1237	ACTGTCCAGGACTGCAACTGTTCATC 1263	

RESULT 6		
LOCUS	HPVJK070A8	
DEFINITION	HPVJK070A8	1584 bp RNA linear
	Hepatitis C virus isolate JK070	VRL 10-FEB-1999
	gene for core, env, and part of	
	E2, NS1, partial cds.	

VERSION	D49752.1	GI:1197162
KEYWORDS	core, env, and part of E2/NS1.	
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	
	viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	

REFERENCE	1 (sites)
AUTHORS	Tokita, H., Okamoto, H., Iizuka, H., Kishimoto, J., Tsuda, F., Lemana, U.A., Miyakawa, Y. and Mayumi, M.
TITLE	Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups
JOURNAL	J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE	96226020
PUBMED	8637233
REFERENCE	2 (bases 1 to 1584)
AUTHORS	Okamoto, H.
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1584)
AUTHORS	Okamoto, H.
TITLE	Direct Submission
JOURNAL	Submitted (17-MR-1995) Hiroaki Okamoto, Jichi Medical School, Immunology Division, 1-8-1, Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail: hokamoto@jichi.ac.jp, Tel: 0285-44-2111 (ex.3334), Fax: 0285-44-1537)
FEATURES	
Source	1. 1584 Location/Qualifiers

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Db	937	CTCTACATATTAACCAACGACTGTAAGCAACGCAATTTGTATATAGGCGGGGGAATTT	996
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QY 421 ACTGTCAGAGACTGCAACTGTTCCATC 447
Db 1237 ACTGTCAGAGATTTGCAACTGTTCCATC 1263

RESULT 8
HPCJK030A3 1584 bp RNA linear VRL 10-FEB-1999
LOCUS Hepatitis C virus isolate JK030 gene for core, env, and part of
DEFINITION E2/NS1, partial cds.
ACCESSION D49747.1 GI:1197102
VERSION D49747.1 GI:1197102
KEYWORDS core, env, and part of E2/NS1.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases)
AUTHORS Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,
Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE Hepatitis C virus variants from Jakarta, Indonesia classifiable
into novel genotypes in the second (2e and 2f), tenth (10a) and
eleventh (11a) genetic groups
JOURNAL J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE 96226020
PUBMED 8627233
REFERENCE 2 (bases 1 to 1584)
AUTHORS Okamoto,H.
TITLE Unpublished
AUTHORS (bases 1 to 1584)
Okamoto,H.
JOURNAL Direct Submission
SUBMITTED (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; MinamiKawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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QY 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTATCTTCTTCG 60

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QY 61 GCTTTGTTCTATGTTGTTGTTTACACCCACAGCGGGCTGAGTACCTTAATGCTCCGGA 120
Db 877 GCTTTGTTCTATGTTGTTGTTTACACCCACAGCGGGCTGAGTACCTTAATGCTCCGGA 936
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Db 1057 ACCTCTGTAAGCCCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1116
QY 301 ACGCAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
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QY 361 CTTTGTGAGCGCGTATTTCTGTGTGGGACGGGGTTCATGAGACATGCCAGCATTTGG 420
Db 1177 CTTTGTGAGCGCGTATTTCTGTGTGGGACGGGGTTCATGAGACATGCCAGCATTTGG 1236
QY 421 ACTGTCAGAGACTGCAACTGTTCCATC 447
Db 1237 ACTGTCAGAGATTTGCAACTGTTCCATC 1263

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DEFINITION E2/NS1, partial cds.
ACCESSION D49753
VERSION D49753.1 GI:1197124
KEYWORDS core, env, and part of E2/NS1.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases)
AUTHORS Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,
Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE Hepatitis C virus variants from Jakarta, Indonesia classifiable
into novel genotypes in the second (2e and 2f), tenth (10a) and
eleventh (11a) genetic groups
JOURNAL J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE 96226020
PUBMED 8627233
REFERENCE 2 (bases 1 to 1584)
AUTHORS Okamoto,H.
TITLE Unpublished
AUTHORS (bases 1 to 1584)
Okamoto,H.
JOURNAL Direct Submission
SUBMITTED (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; MinamiKawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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Best Local Similarity 91.5%; Pred. No. 1,1e-93;
Matches 409; Conservative 3; Mismatches 35; Indels 0; Gaps 0;

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Query Match      86.8%; Score 388.2; DB 14; Length 1584;
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QY 61 GCTTTGTTCTCATGCTTGTAGACCAACGCGGGCTGAGTACCGTATAGCTCCGA 120
DB 877 GCTTTACTCATGCTTGTAGACCAACGCGGGCTGAGTACCGTATACGCTCCGA 936
QY 121 CTCTACATGTAATTAACGACTGACAGTACGTAAGTATCGTATAGAGCGGGGATAT 180
DB 937 CTCTACATGTAATTAACGACTGACAGTACGTAAGTATCGTATAGAGCGGGGATAT 996
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QY 301 ACCGACGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 1117 ACCGACGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1176
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DB 1177 CTTTGTGAGCGATATTTCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1236
QY 421 ACTGTCCAGAGCTGCAACTGTTCCATC 447
DB 1237 ACTGTTCAGAGGAGTCAACTGTTCCATC 1263

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RESULT 10

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HPCP3      411 bp      RNA      linear      VRL 07-FEB-1999
LOCUS      Hepatitis C virus (individual isolate Td-3/93) gene for polypeptide
DEFINITION precursor, partial cds (core protein (carboxy terminus) and E1
envelope protein (amino terminus half)).
ACCESSION  D30046
VERSION    D30046.1 GI:485798
KEYWORDS  E1 envelope protein; core protein.
SOURCE    Hepatitis C virus
ORGANISM  Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
1 (ntee)

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REFERENCE

Hotte,H., Handajani,R., Lusida,M.I., Soemarto,W., Doi,H.,
 Miyajima,H. and Homma,M.
 Subtype analysis of hepatitis C virus in Indonesia on the basis of
 NS5b region sequences
 JOURNAL U. Clin. Microbiol. 32 (12), 3049-3051 (1994)
 MEDLINE 95189942

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PUBMED      7883898
REFERENCE 2 (bases 1 to 411)
AUTHORS   Hotte,H.
JOURNAL   Unpublished
REFERENCE 3 (bases 1 to 411)
AUTHORS   Hotte,H.
TITLE     Direct Subtyping
JOURNAL   Submitted (28-Apr-1994) Hak Hotte, Kobe University School of
Medicine, Department of Microbiology, 7-5-1 Kusunoki-cho, Chuo-ku,
Kobe, Hyogo 650, Japan (Tel:078-341-7451(ex.3301),
Fax:078-351-6347)
COMMENT   Submitted (28-Apr-1994) to DDBJ by:
Hak Hotte
Kobe University School of Medicine
Department of Microbiology
7-5-1 Kusunoki-cho, Chuo-ku
Kobe, Hyogo 650
Japan
Phone: 078-341-7451 X3301
Fax: 078-351-6347.

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DB 62 TGGTAAACAAACGACGACAGTAAACGAGTATGATGATGATGATGATGATGATGATG 121
QY 188 ACTTACCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
DB 122 ACATGCTGTGCTGTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
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QY 428 AGGACTGCACTGTTCCATC 447
DB 362 AGGATTGCAACTGTTCCATC 381

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RESULT 11

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ACCESSION D16614
VERSION D16614.1 GI:475866
KEYWORDS E2/NS1; core protein; envelope protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE
AUTHORS 1 (sites)
TITLE Shrestha, S.M., Tsuda, F., Okamoto, H., Tokita, H., Horikita, M.,
Tanaka, T., Miyakawa, Y., and Mayumi, M.
Hepatitis B virus subtypes and hepatitis C virus genotypes in
patients with chronic liver disease in Nepal
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
JOURNAL Hepatology 19 (4), 805-809 (1994)
MEDLINE 9418615
PUBMED 8138250
2 (sites)
TITLE Tokita, H., Shrestha, S.M., Okamoto, H., Sakamoto, M., Horikita, M.,
Iizuka, H., Shrestha, S., Miyakawa, Y., and Mayumi, M.
Hepatitis C virus variants from Nepal with novel genotypes and
their classification into the third major group
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
JOURNAL 94201770
MEDLINE 8151307
PUBMED
COMMENT Submitted (06-JUN-1993) to DDBJ by:
Hiroaki Okamoto
Immunology Division
Jichi Medical School
Kawachi-gun
Tochigi-ken 329-04
Japan
Phone: 0285-44-2111 x3334
Fax: 0285-44-1557.
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QY 361 CTTTGTGAGGCTATTTCTTGTGCGAGGCGGTTCTATGAGAGCATGCGACATGG 420
DB 1098 TTGTGCGGCGCTTGTCTGTGTGCGAGGCGGTTCTATGAGAGCTGCGAATATT 1157
QY 421 ACTGTCCAGACTGCACTGTTTC 443
DB 1158 ACCGTCCAGTTGTGCAATTTGCTC 1180
RESULT 12
LOCUS HCNE274I 1505 bp RNA linear VRL 10-JUN-1999
DEFINITION Hepatitis C virus RNA for core, env, and part of E2/NS1 polypeptide.
ACCESSION D16620
VERSION D16620.1 GI:475878
KEYWORDS E2/NS1; core protein; envelope protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE
AUTHORS 1 (sites)
TITLE Shrestha, S.M., Tsuda, F., Okamoto, H., Tokita, H., Horikita, M.,
Tanaka, T., Miyakawa, Y., and Mayumi, M.
Hepatitis B virus subtypes and hepatitis C virus genotypes in
patients with chronic liver disease in Nepal
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
JOURNAL Hepatology 19 (4), 805-809 (1994)
MEDLINE 9418615
PUBMED 8138250
2 (sites)
TITLE Tokita, H., Shrestha, S.M., Okamoto, H., Sakamoto, M., Horikita, M.,
Iizuka, H., Shrestha, S., Miyakawa, Y., and Mayumi, M.
Hepatitis C virus variants from Nepal with novel genotypes and
their classification into the third major group
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
JOURNAL 94201770
MEDLINE 8151307
PUBMED
COMMENT Submitted (06-JUN-1993) to DDBJ by:
Hiroaki Okamoto
Immunology Division
Jichi Medical School
Kawachi-gun
Tochigi-ken 329-04
Japan
Phone: 0285-44-2111 x3334
Fax: 0285-44-1557.
LOCATION/Qualifiers
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Tochigi-ken 329-04
Japan
Phone: 0285-44-2111 X3334
Fax: 0285-44-1557.

FEATURES

source

Location/Qualifiers

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5'UTR

CDS

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Best Local Similarity 71.3%; Pred. No. 8.3e-54;
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DEFINITION partial cds.
ACCESSION U39298
VERSION U39298.1
KEYWORDS GI:845459

SOURCE

ORGANISM

Hepatitis C virus type 3a

Hepatitis C virus type 3a

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Hepatitis virus.

1 (bases 1 to 447)

van Doorn, L.J., Klever, B., Stuyver, L., Maertens, G., Brouwer, H.,

Schalm, S.W., Heijlink, R. and Quint, W.G.

Analysis of hepatitis C virus genotypes by a line probe assay and

correlation with antibody profiles

J. Hepatol. 21 (1), 122-125 (1994)

MEDLINE 95052487

PUBMED 7525693

2 (bases 1 to 447)

van Doorn, L.J., Klever, G.B., Stuyver, L., Maertens, G., Brouwer, J.T.,

Schalm, S.W., Heijlink, R.A. and Quint, W.G.

Sequence analysis of hepatitis C virus genotypes 1 to 5 reveals

multiple novel subtypes in the Benelux countries

J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995)

MEDLINE 97201609

PUBMED 9049395

FEATURES

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Location/Qualifiers

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TDCNSNIVYADVDVILHTPBCIPICDQDSTSCMPVPTVAVKVGATTAIRSH

VDLVGATMCSALYEDMCAVFLVADAFTRRRRQTVOTCNLSL"

1..96

/product="core protein"

/note="putative"

97..447

/product="e1 protein"

/note="putative"

ORIGIN

Query Match 53.6%; Score 239.4; DB 14; Length 447;
Best Local Similarity 71.1%; Pred. No. 2.4e-53;
Matches 315; Conservative 1; Mismatches 127; Indels 0; Gaps 0;

1 GACGGAATTAATTTCGCAACAGGAAATTAACCTGCTCTTCTCTATCTTCTCTG 60
1 GACGGAATTAATTTCGCAACAGGAAATTAACCTGCTCTTCTCTATCTTCTCTG 60
61 GCTTGTCTCATGCTTGTCTTACACCCAGCCGCGGCTGAGTACCGTAATGCTCCGA 120
61 GCTTGTCTCTCCGCTTGAAGTCCCGGCGTGTGCTAGTACAGAAACAGTCTGCG 120
121 CTCTACATGTAATTAACGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 180
121 CTCTACATGTAATTAACGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 180
181 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
241 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
301 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
301 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
361 ATCTCTCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 361 ATGTGTGGGGCCGCTCTTCCTGTGTGGACAAAGCCTTCATTCAAGCCTCGTGGCAACAA 420

Oy 421 ACTGTCCAGAGACTGTCAACTGTTC 443

Db 421 ACGGTCCAGACTGTTAAGTCTC 443

Search completed: December 29, 2004, 15:21:53
Job time : 2268 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 29, 2004, 13:30:54 ; Search time 355 Seconds
(without alignments)
6609.834 Million cell updates/sec

Title: US-09-851-138c-51

Perfect score: 447
Sequence: 1 gacggatcaatttcgcac.....agactgcactgtccatc 447

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.8	99.7	447	2	AAT27962
2	236.2	52.8	540	2	AAQ78031
3	236.2	52.8	541	2	AAQ78029
4	234.6	52.5	541	2	AAQ78033
5	234.6	52.5	541	2	AAQ78036
6	234.6	52.5	541	2	AAQ78032
7	233	52.1	541	2	AAQ78030
8	233	52.1	541	2	AAQ78034
9	233	52.1	541	2	AAQ78035
10	233	52.1	630	2	AAT12965
11	233	52.1	630	2	AAT12965
12	233	52.1	630	2	AAT12965
13	233	52.1	630	2	AAT12965
14	221.4	49.5	1249	2	AAZ07658
15	219.4	48.6	579	2	AAQ35072
16	217.4	48.3	579	2	AAQ78104
17	216.2	48.4	580	2	AAZ07652
18	215.8	48.3	574	2	AAQ78081
19	215.8	48.3	579	2	AAQ78106
20	215.8	48.3	579	2	AAQ78103
21	209.8	46.9	447	2	AAT27956

22	209	46.8	447	2	AAT27952	AAT27952 Hepatitis
23	208.6	46.7	447	2	AAT27955	AAT27955 Hepatitis
24	206.6	46.2	579	2	AAQ78102	AAQ78102 Hepatitis
25	206.2	46.1	579	2	AAQ78109	AAQ78109 Hepatitis
26	205	45.9	579	2	AAQ78101	AAQ78101 Hepatitis
27	204.6	45.8	574	2	AAQ78080	AAQ78080 Hepatitis
28	204.2	45.7	1270	2	AAV60668	AAV60668 Fragment
29	204.2	45.7	1562	2	AAV60672	AAV60672 Fragment
30	204.2	45.7	1553	8	AAV55222	AAV55222 plasmid P
31	204.2	45.7	2116	2	AAQ12242	AAQ12242 Encodes P
32	204.2	45.7	2829	2	AAV60673	AAV60673 Fragment
33	203	45.4	579	2	AAQ78114	AAQ78114 Hepatitis
34	203	45.4	579	2	AAQ78108	AAQ78108 Hepatitis
35	201.4	45.1	579	2	AAQ78113	AAQ78113 Hepatitis
36	201.4	45.1	579	2	AAQ78093	AAQ78093 Hepatitis
37	201	45.0	447	2	AAT27951	AAT27951 Hepatitis
38	199.4	44.6	673	2	AAV42305	AAV42305 HCV core
39	199.4	44.6	742	2	AAQ20926	AAQ20926 C10-E15 D
40	199.4	44.6	932	2	AAQ20923	AAQ20923 C10-E12 D
41	198.2	44.3	447	2	AAT27954	AAT27954 Hepatitis
42	197.8	44.3	447	2	AAT27953	AAT27953 Hepatitis
43	196.2	43.9	577	2	AAQ35082	AAQ35082 HCV env
44	196.2	43.9	633	2	AAT12706	AAT12706 HCV E1 co
45	196.2	43.9	633	6	AAI48915	AAI48915 Hepatitis

ALIGNMENTS

RESULT 1
AAT27962
ID AAT27962 standard; DNA; 447 BP.
XX
AC AAT27962;
XX
DT 11-MAR-1997 (first entry)
XX
DE Hepatitis C virus type 10a isolate NB98 bases 478-925.
XX
KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;
KW PCR; primer; probe; antibody; infection; ss.
XX
OS Hepatitis C virus.
XX
PN MO9613590-A2.
XX
PD 09-MAY-1996.
XX
PF 23-OCT-1995; 95WO-EP04155.
XX
PR 21-OCT-1994; 94EP-00870166.
PR 28-JUN-1995; 95EP-00870076.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Maertens G, Stuyver L;
XX
DR WPI; 1996-251460/25.
DR P-PSDB; AAR6551.
XX
PT Hepatitis C virus poly:nucleic acid unique to unidentified sub: type -
PT used to develop probes and primers for new sub: types and vaccines to
PT prevent and treat infection.
XX
XX claim 6; Fig 3; 150p; English.
XX
XX The sequences AAT27937-T27989 represent novel sequences isolated from
CC hepatitis C virus subtypes different from subtypes 1a-c, 2a-d, 3a-f, 4a-
CC 1, 5a and 6a. They esp. from the novel subtypes 1d-f, 2e-1, 2k, 2l, 3g,
CC 4k-m, 7a-c or types 9, 10 or 11. The sequences corresp. to the 5'
CC untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.
CC This sequence represents nucleotides 478-925 from the HCV type 10a
CC isolate NB98. The new HCV types were isolated from patients with chronic

CC HCV from the Benelux countries, France, Cameroon and Vietnam, because of
CC their aberrant activities. The RNA was extracted, cDNA synthesised and
CC PCR amplified, cloned and genotyped. The 5'UTR, Core/E1 and NS5B regions
CC were sequenced either directly or partially and used to classify the new
CC viruses into (sub)types based on comparison with known sequences. The
CC sequences were used to generate the peptides AAR6424-R96524. The
CC sequences can also be used to synthesise probes and primers for the
CC detection of HCV in a sample. The polypeptides can be used to detect anti
CC -HCV antibodies, for HCV typing or to prevent HCV infections

XX Sequence 447 BP; 82 A; 130 C; 114 G; 118 T; 0 U; 3 Other;

Query Match 99.7%; Score 445.8; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 1.4e-129;

Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GACGGAATTAATTTGGCAACAGGGAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60
QY 61 GCTTTGTTCTCATGCTTGTGCTTACACCCAGCCGCGGCTGAGTACCGTATGCTCCGGA 120
DB 61 GCTTTGTTCTCATGCTTGTGCTTACACCCAGCCGCGGCTGAGTACCGTATGCTCCGGA 120
QY 121 CTCTACATGATTAATTAACAGCTGCAAGTAAAGGATGATGATGATGATGATGATGAT 180
DB 121 CTCTACATGATTAATTAACAGCTGCAAGTAAAGGATGATGATGATGATGATGATGAT 180
QY 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 ATCCCTGAGAGCCGCTGAGCCGCTGAGAGTGCCTGCGCGCCGCTGCTGCTGCTG 300
DB 241 ATCCCTGAGAGCCGCTGAGCCGCTGAGAGTGCCTGCGCGCCGCTGCTGCTGCTG 300
QY 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 CTTTGTGAGAGCGTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420
DB 361 CTTTGTGAGAGCGTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420
QY 421 ACTGTCAGAGCTGCAACTGTTCCATC 447
DB 421 ACTGTCAGAGCTGCAACTGTTCCATC 447

RESULT 2
AAQ78031
ID AAQ78031 standard; cDNA; 540 BP.
XX
AC AAQ78031;
XX
DT 25-MAR-2003 (revised)
DT 21-JUL-1995 (first entry)
XX
DE Hepatitis C virus Core/E1 region.
XX
KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;
XX classification; immunisation; prophylaxis; serotyping; ss.
XX
OS Hepatitis C virus type 3a.
XX
FH Key Location/Qualifiers
FT CDS 2..541
FT /tag= a
FT /product= "Core/E1 polypeptide."
XX
PN MO9425601-A2.
XX
PD 10-NOV-1994.
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XX 27-APR-1994; 94MO-BP001323.
PF 27-APR-1994; 93EP-00401099.
PR 05-AUG-1993; 93EP-00402019.
XX (INNO-) INNOGENETICS NV SA.
XX
XX Maertens G, Stuyver L;
XX
XX WPI; 1994-358277/44.
DR P-PSDB; AAR63279.
XX
XX New polynucleotide sequences from hepatitis C virus - and related
XX vectors, polypeptide(s) and antibodies, useful for immunisation,
XX treatment, diagnosis and typing of HCV isolates.

Claim 2; Page 107-108; 404pp; English.

Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the Core/E1
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
CC positions 8023-8235 of the NS5 region of the BR56 subgroup of HCV subtype
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
CC amplify nucleic acid from an isolate belonging to a specific genotype, or
CC as a probe for specific detection/classification of nucleic acid.
CC Polypeptides encoded by the nucleotides in such compositions may be used
CC for immunisation against HCV, for the detection of antibodies directed
CC against HCV and for serotyping. This sequence corresponds to the Core/E1
CC region of HCV subtype 3a and is taken from a clone designated HD10-2-21.
XX (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 540 BP; 105 A; 153 C; 144 G; 138 T; 0 U; 0 Other;

Query Match 52.8%; Score 236.2; DB 2; Length 540;

Best Local Similarity 70.7%; Pred. No. 1.1e-63;

Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

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DB 61 GACGGAATTAATTTGGCAACAGGGAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 120
QY 61 GCTTTGTTCTCATGCTTGTGCTTACACCCAGCCGCGGCTGAGTACCGTATGCTCCGGA 120
DB 121 GCTTTGTTCTCATGCTTGTGCTTACACCCAGCCGCGGCTGAGTACCGTATGCTCCGGA 180
QY 121 CTCTACATGATTAATTAACAGCTGCAAGTAAAGGATGATGATGATGATGATGATGAT 180
DB 181 CTCTACATGATTAATTAACAGCTGCAAGTAAAGGATGATGATGATGATGATGATGAT 240
QY 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 241 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 241 ATCCCTGAGAGCCGCTGAGCCGCTGAGAGTGCCTGCGCGCCGCTGCTGCTGCTG 300
DB 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 361 AGGCATGATGATATTTGTTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420
QY 361 CTTTGTGAGAGCGTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420
DB 421 ATGTTGAGAGCGTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 480
QY 421 ACTGTCAGAGCTGCAACTGTTCC 443
DB 481 ACGTCAGAGCTGCAACTGTTCC 503
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RESULT 3
AAQ78029 standard; cDNA, 541 BP.
XX
XX AAQ78029;
AC
XX
XX 25-MAR-2003 (revised)
DT 20-UDL-1995 (first entry)
XX
XX Hepatitis C virus Core/E1 region.
DE
XX
XX Hepatitis C virus; HCV; primer: probe: detection; diagnosis;
KM classification; immunisation; prophylaxis; serotyping; ss.
XX
XX Hepatitis C virus type 3a.
OS
XX
XX Key Location/Qualifiers
FH 2..541
FT CDS /tag= a
FT /product= "Core/E1 polypeptide."
FT
XX
XX MO9425601-A2.
PN 10-NOV-1994.
XX
XX 27-APR-1994; 94MO-BP001323.
XX
XX 27-APR-1993; 93BP-00401099.
PR 05-AUG-1993; 93BP-00402019.
XX
XX (INNO-) INNOGENETICS NV SA.
PA
XX Maertens G, Stuyver L;
PI
XX WPI; 1994-358277/44.
DR P-PSDB; AAR63277.
XX
XX New polynucleotide sequences from hepatitis C virus - and related
PT vectors, polypeptide(s) and antibodies, useful for immunisation,
PT treatment, diagnosis and typing of HCV isolates.
XX
XX Claim 2; Page 103-104; 404pp; English.
XX
XX Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the Core/E1
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
CC amplify nucleic acid from an isolate belonging to a specific genotype, or
CC as a probe for specific detection/classification of nucleic acid.
CC Polypeptides encoded by the nucleotides in such compositions may be used
CC for immunisation against HCV, for the detection of antibodies directed
CC against HCV and for serotyping. This sequence corresponds to the Core/E1
CC region of HCV subtype 3a and is taken from a clone designated HD10-2-5.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 541 BP; 104 A; 153 C; 145 G; 139 T; 0 U; 0 Other;
SO
Query Match 52.8%; Score 236.2; DB 2; Length 541;
Best Local Similarity 70.7%; Pred. No. 1.1e-63;
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;
XX
OY 1 GACGGAATTAATTCGACAGGGAATTTACTGCTGCTTCTTCTATCTTCCTTCG 60
DB 62 GACGGATTAATTCGACAGGGAATTTCTCCGTTCTCTTCTATCTTCCTTCCTT 121
OY 61 GCTTTGTTCTATGCTTGTACACCCAGCCGCGGTGAGTACCGTAATGCTCCGGA 120
DB 122 GCTCTGTTCTTCTTATTCATCCAGCAGCTAAGTCTAAGTGGGGAACAGCTGGC 181

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OY 121 CTCTAATGTAATTAACAGATGACGTAACGTAAGTAATGTAAGGACCGGATATT 180
DB 182 CTCTAATGTAATTAACAGATGTAACGTAATGTAAGTAAGGACCGGATATT 241
OY 181 ATCTCCACTTACCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 242 ATTCTGCAACACCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
OY 241 ATCTCTGAGCCCTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 302 ACCCCAGTACACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
OY 301 ACCGAGTGAATATGATGTAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 362 AGGATGTAAGATGTAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421
OY 361 CTCTGAGAGGCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 422 ATGTGTGGGCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
OY 421 ACTGTCAGAGACTGCAACTGTTTC 443
DB 482 ACGTCCAGACCTGTAATGCTC 504

RESULT 4
AAQ78033 standard; cDNA, 541 BP.
XX
XX AAQ78033;
AC
XX
XX 25-MAR-2003 (revised)
DT 01-AUG-1995 (first entry)
XX
XX Hepatitis C virus Core/E1 region.
DE
XX
XX Hepatitis C virus; HCV; primer: probe: detection; diagnosis;
KM classification; immunisation; prophylaxis; serotyping; ss.
XX
XX Hepatitis C virus type 3a.
OS
XX
XX Key Location/Qualifiers
FH 2..541
FT CDS /tag= a
FT /product= "Core/E1 polypeptide."
FT
XX
XX MO9425601-A2.
PN 10-NOV-1994.
XX
XX 27-APR-1994; 94MO-BP001323.
XX
XX 27-APR-1993; 93BP-00401099.
PR 05-AUG-1993; 93BP-00402019.
XX
XX (INNO-) INNOGENETICS NV SA.
PA
XX Maertens G, Stuyver L;
PI
XX WPI; 1994-358277/44.
DR P-PSDB; AAR63281.
XX
XX New polynucleotide sequences from hepatitis C virus - and related
PT vectors, polypeptide(s) and antibodies, useful for immunisation,
PT treatment, diagnosis and typing of HCV isolates.
XX
XX Claim 2; Page 111-112; 404pp; English.
XX
XX Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the Core/E1
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of

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CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
CC amplify nucleic acid from an isolate belonging to a specific genotype, or
CC as a probe for specific detection/classification of nucleic acid.
CC Polypeptides encoded by the nucleotides in such compositions may be used
CC for immunisation against HCV, for the detection of antibodies directed
CC against HCV and for serotyping. This sequence corresponds to the Core/E1
CC region of HCV subtype 3a and is taken from a clone designated BR36-9-20.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 106 A; 154 C; 142 G; 139 T; 0 U; 0 Other;

Query Match 52.5%; Score 234.6; DB 2; Length 541;

Best Local Similarity 70.4%; Pred. No. 3.6e-63;

Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGAAATTAACCTGTGCTCTTCTATCTTCTCTG 60
DB 62 GACGGGATTAATTTCGCAACAGGAAATTAACCTGTGCTCTTCTATCTTCTCTG 121
QY 61 GCTTTGTTCTATCTTCTGCTTACACCAACAGCGGCTGGAGTACCTTAATGCTCCGA 120
DB 122 GCTGTGTTCTCTGCTTAAATTCATCCAGAGCTAGTCTAGAGTGGCGGAATAGCTCTGC 181
QY 121 CTCTACATGATTAACAGCACTGAGTAACGGTAGTATGCTGATAGAGCCGGGATAT 180
DB 182 CTCTAGTCTCTTACCAACAGCTGTTCCAAATAGAGATGTTGTACAGAGCCATGACGTT 241
QY 181 ATCTCTCACTTAACCTGCTGTGTCCCTGCGTACGCTCTGCAATACATCAAGATCTG 240
DB 242 ATCTCTCAACACCCGCTGTATACCTTGTGTACAGAGCGCAATATCACTACGCTCG 301
QY 241 ATCCCTGTAGACCCCTACCGTCCGCTGGAAGTGCCTCTGGCCGCCACCGCTCTCTCCG 300
DB 302 ACCCGAGTACACTACAGTGCAGTCAAGTACGTGAGCAACACCGCTCTGATACGC 361
QY 301 ACSCAGTGAATATGATGTGGGAGCGGCCACCTATGCTAGCTCTTACGTAAGAGAC 360
DB 362 AGTCATGTGAGCACTTATTAAGTGGCGCGGCCACAGATGCTCTGCTTACGTTGGTGC 421
QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATAGACATCGCCAGCATTTG 420
DB 422 ATGTGTGGGGGCTGTCTCTCGTGGGACAAGCCTTACGTTGAGACCTCGTGTATCA 481
QY 421 ACTGTCCAGACTGCAACTGTTTC 443
DB 482 ACGGTCCAGACTGTAACGTGCTC 504

RESULT 5

AAQ78036 standard; cDNA; 541 BP.

XX AAQ78036;

XX 25-MAR-2003 (revised)

XX 01-AUG-1995 (first entry)

XX Hepatitis C virus Core/E1 region.

XX Hepatitis C virus; HCV; primer; probe; detection; diagnosis;

XX classification; immunisation; prophylaxis; serotyping; ss.

XX Hepatitis C virus type 3a.

XX Key

XX Location/Qualifiers

XX CDS 2..541

XX /tag= a

XX /product= "Core/E1 polypeptide."

XX

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XX 10-NOV-1994.

PD 27-APR-1994; 94MO-EP001323.

XX 27-APR-1993; 93EP-00401099.

XX 05-AUG-1993; 93EP-00402019.

XX (INNO-) INNOGENETICS NV SA.

PA Maertens G, Stuyver L;

PI WPI; 1994-358277/44.

XX P-PSDB; AAR63284.

XX

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ID	Accession	Standard	CDNA	Size (BP)
RESULT 6	AAQ78032	standard	CDNA	541 BP.
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AC	AAQ78032			
XX				
DT	25-MAR-2003	(revised)		
DT	01-AUG-1995	(first entry)		
XX				
DE	Hepatitis C virus Core/E1 region.			
XX				
KM	Hepatitis C virus; HCV; primer; probe; detection; diagnosis;			
KM	classification; immunisation; prophylaxis; serotyping; ss.			
OS	Hepatitis C virus type 3a.			
XX				
PH	Key	Location/Qualifiers		
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FT		/*tag= a		
XX		/product= "Core/E1 polypeptide."		
PN	MO9425601-A2.			
PD	10-NOV-1994.			
XX				
PF	27-APR-1994;	94WO-EP001323.		
PR	27-APR-1993;	93EP-00401099.		
PR	05-AUG-1993;	93EP-00402019.		
XX				
PA	(INNO-) INNOGENETICS NV SA.			
PI	Maertens G, Stuyver L;			
XX				
DR	WPI; 1994-358277/44.			
XX	P-PSDB; AAR63280.			
XX				
PT	New polynucleotide sequences from hepatitis C virus - and related			
PT	vectors, polypeptide(s) and antibodies, useful for immunisation,			
XX	treatment, diagnosis and typing of HCV isolates.			
PS	Claim 2; Page 109-110; 404pp; English.			
XX				
CC	Compositions comprising at least 5, and pref. 8 or more contiguous			
CC	nucleotides selected from an HCV type 3 genomic sequence, more			
CC	particularly (i) the region spanning positions 417-957 of the Core/E1			
CC	region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of			
CC	the NS3 region of HCV type 3; (iii) the region spanning positions 4892-			
CC	5292 of the NS3/4 region of HCV type 3; (iv) the region spanning			
CC	positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype			
CC	3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to			
CC	amplify nucleic acid from an isolate belonging to a specific genotype, or			
CC	as a probe for specific detection/classification of nucleic acid.			
CC	Polypeptides encoded by the nucleotides in such compositions may be used			
CC	for immunisation against HCV, for the detection of antibodies directed			
CC	against HCV and for serotyping. This sequence corresponds to the Core/E1			
CC	region of HCV subtype 3a and is taken from a clone designated BR36-9-13.			
CC	(Updated on 25-MAR-2003 to correct PN field.)			
XX				
XX	Sequence 541 BP; 107 A; 155 C; 142 G; 137 T; 0 U; 0 Other;			
XX				
Query Match	52.5%;	Score 234.6;	DB 2;	Length 541;
Beet Local Similarity	70.4%;	Pred. No. 3.6e-63;		
Matches 312;	Conservative 1;	Mismatches 130;	Indels 0;	Gaps 0
1	GACGGAATTAATTTGCGCAACAGGGAATTAACCTGTTGCTCTTCTATCTTCCTTCG 60			
62	GACGGGATTAATTTGCGCAACAGGGAATTTGCCGGTGTGCTCTTCTATTTTCCTTCT 121			
61	GCTTTGTTCTATGCTGCTTACACCCAGCCGGGCTGAGTACCGTAATGCTTCGGA 120			

Dd		122	GCTCTGTTTCTTGCTTAATTATCAGACAGCTAGTCAGAGTGCGGGAAATAGCTCCGC	181
Oy		121	CTCAACAATGGATACTAAGCATGTGCAAGTAACGGTAGTATGCTGTATGAAGCCGGGGAATTT	180
Dd		182	CTGTATGTCTTAAACCAACGACTGTTCCAATAGCAGTATTGTGTGAGGCCGATGACGTT	241
Oy		181	ATCTCTCACACTAACCTGGCGTGTGTCCCCTGCGCAAGCTGTGGCAATPACAATCAAGATGCTGG	240
Dd		242	ATTCTGTACACACCACCGGCTGTACATCTTGTGTCCAGAGCGGCAATPACATCCACGTGCTGG	301
Oy		241	ATCTCTGTGAGCCCVACCGTCGCGCTGTGAAGTGTGCGCTTGCSCGCGCACCGCCTCTCTCCGC	300
Dd		302	ACCCCACTGACACTTCACTAGTGGCAATGCAAGTACGTGCGSAGCAACACCGCTTGATACGC	361
Oy		361	ACGCACGTGATATGATGTGTGGGRRCGGCGCACCTTAGCTCAGCTCTCTTACGTAGAAGAC	360
Dd		362	AGTCATGTGGACTATTATTAATGTGGCGCGGCGCAAGATGTCTCAGCGCTCTACGTGGGTGAT	421
Oy		422	CTTTGTGAGACGGCTATTTTGTGTGGCGAGGGGTTCTCATATGGAAPACATCCGACGATTGG	420
Dd		421	ATGTGTGGGGCGCTCTTCTTGTGTGGGACAAAGCCTTCACGTTCAAGACCTGTGCGCAATA	481
Oy		421	ACTGTCCAGGACTGCACACTGTTC	443
Dd		482	ACGGTCCAGACTGTAACTGCTC	504
RESULT 7				
AAQ78030				
ID	AAQ78030	standard; cDNA; 541 BP.		
XX	AAQ78030;			
AC				
XX	25-MAR-2003 (revised)			
DT	21-JUL-1995	(first entry)		
XX				
Dd	Hepatitis C virus Core/EI region.			
XX				
Dd	Hepatitis C virus; HCV; primer; probe; detection; diagnosis;			
KW	classification; immunisation; prophylaxis; serotyping; ss.			
XX				
OS	Hepatitis C virus type 3a.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	2..541		
FT		/tag= a		
FT		/product= "Core/EI polypeptide."		
FN	W09425601-A2.			
XX				
PD	10-NOV-1994.			
XX				
PE	27-APR-1994;	94MO-BE001323.		
XX				
PR	27-APR-1993;	93BP-00401099.		
PR	05-AUG-1993;	93BP-00402019.		
XX				
PA	(INNO-) INNOGENETICS NV SA.			
XX				
FI	Maertens G, Stuyver L;			
DR	WPI; 1994-358277/44.			
DR	P-PSDB; AAF63278.			
XX				
PT	New polynucleotide sequences from hepatitis C virus - and related			
PT	vectors, polypeptide(s) and antibodies, useful for immunisation,			
XX	treatment, diagnosis and typing of HCV isolates.			
XX				
PS	Claim 2; Page 105-106; 404pp; English.			
CC	Compositions comprising at least 5, and pref. 8 or more contiguous			
CC	nucleotides selected from an HCV type 3 genomic sequence, more			

CC particularly (i) the region spanning positions 417-957 of the Core/EI
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
CC amplify nucleic acid from an isolate belonging to a specific genotype, or
CC as a probe for specific detection/classification of nucleic acid.
CC Polypeptides encoded by the nucleotides in such compositions may be used
CC for immunisation against HCV, for the detection of antibodies directed
CC against HCV and for serotyping. This sequence corresponds to the Core/EI
CC region of HCV subtype 3a and is taken from a clone designated HD10-2-14.
CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 106 A; 154 C; 143 G; 138 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;
Best Local Similarity 70.2%; Pred. No. 1.1e-62;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTGGCAAGGGAATTTACCGTGGTCTTCTATCTTCTCTCG 60
DB 62 GACGGAAATTAATTTGGCAAGGGAATTTGCGGTTGCTCTTCTATCTTCTCTCT 121
QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGAGTACCGTATGCTCCGA 120
DB 122 GCTTGTCTCTTCTTCTTATTCATCCAGCAGTATGCTAGAGTGGGGAACAGTCTGCG 181
QY 121 CTCTACATGATGTAACGACAGTCAAGTACGATGATGATGATGATGATGATGATGAT 180
DB 182 CTCTATGTCCTTACCAACGACGCTGTCATAGCAATGATGATGATGATGATGATGATG 241
QY 181 ATCCCTCACCTTACCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 242 ATTTCTCAACACCCGCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
QY 241 ATCCCTGTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 302 ACCCGAGTACACCTTACGAGTGGCAGTCAAGTATGCTGCTGCTGCTGCTGCTGCTGCT 361
QY 301 AGCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 362 AGCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 361 CTCTTGTGAGCGCTTATTTCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 422 ATGTGTGGGCGCTCTTCTCTGTGGACAAGCTTACGTTACGACCTGTGCGCATCA 481
QY 421 ACTGTCCAGAGCTGCAACTGTTC 443
DB 482 ACGGTCCAGACCTGTAACTGCTC 504

RESULT 8
AAQ78034
ID AAQ78034 standard; cDNA; 541 BP.
XX

AC AAQ78034;
XX
DT 25-MAR-2003 (revised)
DT 01-AUG-1995 (first entry)
XX
DE Hepatitis C virus Core/EI region.
XX
KM Hepatitis C virus; HCV; primer, probe, detection; diagnosis;
KM classification; immunisation; prophylaxis; serotyping; ss.
XX
OS Hepatitis C virus type 3a.

XX Key Location/Qualifiers
FH CDS 2..541
FT /stage a
FT /product= "Core/EI polypeptide."

XX
PN MO9425601-A2.

XX 10-NOV-1994.

XX 27-APR-1994; 94WO-BP001323.

XX 27-APR-1993; 93BP-00401099.

XX 05-AUG-1993; 93BP-00402019.

XX (INNO-) INNOGENETICS NV SA.

XX Maertens G, Stuyver L;

XX WPI; 1994-358277/44.

XX P-PsDB; AAR63282.

XX New polynucleotide sequences from hepatitis C virus - and related
XX vectors, polypeptide(s) and antibodies, useful for immunisation,
XX treatment, diagnosis and typing of HCV isolates.

XX Claim 2, Page 113-114, 404pp; English.

CC Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the Core/EI
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
CC amplify nucleic acid from an isolate belonging to a specific genotype, or
CC as a probe for specific detection/classification of nucleic acid.
CC Polypeptides encoded by the nucleotides in such compositions may be used
CC for immunisation against HCV, for the detection of antibodies directed
CC against HCV and for serotyping. This sequence corresponds to the Core/EI
CC region of HCV subtype 3a and is taken from a clone designated BR33-1-10.
CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 100 A; 157 C; 148 G; 136 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;
Best Local Similarity 70.2%; Pred. No. 1.1e-62;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTGGCAAGGGAATTTACCGTGGTCTTCTATCTTCTCTCG 60
DB 62 GACGGAAATTAATTTGGCAAGGGAATTTGCGGTTGCTCTTCTATCTTCTCTCT 121
QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGAGTACCGTATGCTCCGA 120
DB 122 GCTTGTCTCTTCTTCTTATTCATCCAGCAGTATGCTAGAGTGGGGAACAGTCTGCG 181
QY 121 CTCTACATGATGTAACGACAGTCAAGTACGATGATGATGATGATGATGATGATGATG 180
DB 182 CTCTATGTCCTTACCAACGACGCTGTCATAGCAATGATGATGATGATGATGATGATG 241
QY 181 ATCCCTCACCTTACCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 242 ATTTCTCAACACCCGCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
QY 241 ATCCCTGTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 302 ACCCGAGTACACCTTACGAGTGGCAGTCAAGTATGCTGCTGCTGCTGCTGCTGCTGCT 361
QY 301 AGCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 362 AGTCAATGATGACCTGTATGATGAGCGCGGCAAGATGCTGTGCGCTTACGATGATG 421
QY 361 CTCTTGTGAGCGCTTATTTCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 422 ATGTGTGGGCGCTCTTCTCTGTGGACAAGCTTACGTTACGACCTGTGCGCATCA 481

CC constructs containing the purified HCV envelope proteins can be used for
CC vaccinating humans against HCV, for in vitro detection of HCV antibodies
CC in a sample, and in a serotyping assay for detecting one or more
CC serological types of HCV present in a biological sample. The constructs
CC can also be immobilised on a solid substrate and incorporated into a
CC reversed phase hybridisation assay for determining the presence or the
CC genotype of HCV. The new purification method preserves the conformation
CC of the recombinantly expressed E1, E2 and E1/E2, and eliminates
CC contaminating proteins. Antigens isolated using this method are more
CC reactive with human sera than those isolated by known techniques
XX

Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 630;
Best Local Similarity 70.2%; Pred. No. 1.2e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGGAATTTAAGTGTGCTCTTCTCTATCTTCTCTG 60
DB 124 GACGGGATTAATTTCCCAACAGGGAATTTGCCGGTGTGCTCTTCTATTTCTCTTC 183
QY 61 GCTTGTCTCAATGCTTGTGCTTACCCACAGCGCGGCTGGAGTACCGTATGCTCCGA 120
DB 184 GCTCTGTCTCTGCTTAAATTAATCAAGCAAGCTAGTCTAGAGTGGCGAATATGCTGCG 243
QY 121 CTCTACATGTAATTAACAGCACTGCAAGTAAAGTATGATGATGAGCCGGGATATT 180
DB 244 CTCTATGTCCTTACCAACAGCACTGTTCCAAATAGAGATTTGTAGAGGCCCATGACGT 303
QY 181 ATCTTCACTTAATCTGCTGTGTGCTCCCTGCGTACGCTCTGGCAATATCAATCAAGATCTG 240
DB 304 ATTTTCACACACACCCGGCTGCATACCTTGTGTCCAGAGCGGCAATTCATCAAGTCTG 363
QY 241 ATCCCTGTAGAGCCGTCACCGTGCAGAGTGTGCGTGGCGCGCCACCGCTCTCCGCG 300
DB 364 ACCCCAGTACACTTCAAGTGCAGTCAAGTACGTGAGCAACACCGCTTGTGATACG 423
QY 301 ACGCAGTGAATATGATGTGGGCGGCCACCTTATGCTCAAGCTCTTACATGAGAGAC 360
DB 424 AGTCATGTGACCTATTAGTGGGCGGCGCAGATGTGCTGCTTACGTGGTGAC 483
QY 361 CTTTGTGAGAGCGTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCCAGCATTTG 420
DB 484 ATGTGTGGGGCTGTCTTCTCGTGGGCAAGCCTTCAAGCTTCAGACCTGTCGCGCATCA 543
QY 421 ACTGTCCAGAGACTGCAACTGTTTC 443
DB 544 ACGGTCCAGACTGTAACTGCTC 566

RESULT 11

AA148929
ID AA148929 standard; DNA; 630 BP.

XX AC AA148929;

XX DT 24-OCT-2002 (first entry)

XX DE Hepatitis C virus clone HCC162 E1 protein coding sequence.

XX KW Hepatitis C virus; HCV; E1 protein; E2 protein; infection; gene;
XX virucide; immunostimulant; vaccine; ds.

XX OS Hepatitis C virus.

XX PN WO20025548-A2.

XX PD 18-JUL-2002.

XX PF 11-JAN-2002; 2002WO-BP000219.

XX PR 11-JAN-2001; 2001US-0260669P.
XX PR 30-AUG-2001; 2001US-0315768P.

XX (INNO-) INNOGENETICS NV.

XX PA Maertens G, Bosman F, Buysse M;

XX DR WPI; 2002-59657/64.

XX DR P-PSDB; AAO18670.

XX PT New therapeutic vaccine compositions comprising at least one purified
XX recombinant hepatitis C virus (HCV) single or specific oligonucleic
XX recombinant envelope protein E1 or E2, useful for immunizing humans from
XX HCV infection.

XX Example 2; Page 181-182; 243pp; English.

XX The present invention relates to new therapeutic vaccine compositions for
XX inducing hepatitis C virus (HCV)-specific antibodies, comprising a
XX composition containing at least one purified recombinant HCV single or
XX specific oligonucleic recombinant envelope proteins selected from an E1 and
XX an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
XX useful for inducing HCV-specific antibodies or for immunising humans
XX against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
XX vaccines or therapeutics, in HCV screening and confirmatory antibody
XX tests, for raising antibodies, in the preparation of medicament, and for
XX in vitro monitoring of HCV disease or prognosing the response to
XX treatment of patients suffering from HCV infection. The present sequence
XX is a coding sequence described in the exemplification of the invention

Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 6; Length 630;
Best Local Similarity 70.2%; Pred. No. 1.2e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGGAATTTAAGTGTGCTCTTCTCTATCTTCTCTG 60
DB 124 GACGGGATTAATTTGGCAACAGGGAATTTGCCGGTGTGCTCTTCTATTTCTCTTC 183
QY 61 GCTTGTCTCAATGCTTGTGCTTACCCACAGCGCGGCTGGAGTACCGTATGCTCCGA 120
DB 184 GCTCTGTCTCTGCTTAAATTAATCAAGCAAGCTAGTCTAGAGTGGCGAATATGCTGCG 243
QY 121 CTCTACATGTAATTAACAGCACTGCAAGTAAAGTATGATGATGAGCCGGGATATT 180
DB 244 CTCTATGTCCTTACCAACAGCACTGTTCCAAATAGAGATTTGTAGAGGCCCATGACGT 303
QY 181 ATCTTCACTTAATCTGCTGTGTGCTCCCTGCGTACGCTCTGGCAATATCAATCAAGATCTG 240
DB 304 ATTTTCACACACACCCGGCTGCATACCTTGTGTCCAGAGCGGCAATTCATCAAGTCTG 363
QY 241 ATCCCTGTAGAGCCGTCACCGTGCAGAGTGTGCGTGGCGCGCCACCGCTCTCCGCG 300
DB 364 ACCCCAGTACACTTCAAGTGCAGTCAAGTACGTGAGCAACACCGCTTGTGATACG 423
QY 301 ACGCAGTGAATATGATGTGGGCGGCCACCTTATGCTCAAGCTCTTACATGAGAGAC 360
DB 424 AGTCATGTGACCTATTAGTGGGCGGCGCAGATGTGCTGCTTACGTGGTGAC 483
QY 361 CTTTGTGAGAGCGTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCCAGCATTTG 420
DB 484 ATGTGTGGGGCTGTCTTCTCGTGGGCAAGCCTTCAAGCTTCAGACCTGTCGCGCATCA 543
QY 421 ACTGTCCAGAGACTGCAACTGTTTC 443
DB 544 ACGGTCCAGACTGTAACTGCTC 566

RESULT 12

ADDS5537
ID ADDS5537 standard; DNA; 630 BP.

XX AC ADDS5537;

DT 15-JAN-2004 (first entry)
 XX Hepatitis C virus E1/E2 protein coding sequence #5.
 DE
 XX Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
 KM liver fibrosis; ds, gene.
 XX
 OS Hepatitis C virus.
 PN WO2003051912-A2.
 PD 26-JUN-2003.
 XX
 PF 18-DEC-2002; 2002MO-EP014480.
 XX
 PR 18-DEC-2001; 2001US-00020510.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (INNO-) INNOGENETICS NV.
 PI Maertens G, Depla E, Bosman F;
 XX WPI; 2003-541632/51.
 DR P-PSDB; ADD55538.
 XX
 PT New hepatitis C virus (HCV) vaccine composition, useful for reducing
 XX liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
 PS Example 2; SEQ ID NO 29; 271pp; English.
 CC The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
 CC liver disease. The vaccine of the invention comprises an HCV E1 or E2
 CC protein as an antigen. The HCV vaccine is useful for reducing liver
 CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
 CC present DNA sequence encodes an HCV E1/E2 protein.
 XX
 SQ Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;
 Query Match 52.1%; Score 233; DB 10; Length 630;
 Best Local Similarity 70.2%; Pred. No. 1.2e-62;
 Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;
 QY 1 GAGGGAATTAATTCGACAGGAGGAAATTAATTCGTTGCTTCTTCTATCTCTCTG 60
 DB 124 GAGGGAATTAATTCGACAGGAGGAAATTAATTCGTTGCTTCTTCTATCTCTCTG 183
 QY 61 GCTTGTCTCATGCTTGTGTTACACCAAGCCGCGGTGAGTACGTAATGCTCGGA 120
 DB 184 GCTGTGTCTCTGCTTAATTCATCCAGCAGCTAGTGAAGTGGCGGAATACGTCGCG 243
 QY 121 CTTCATAGGTAACTAACAAGCTCAAGTACGTAATCTGTATGAGGCGGAGATATT 180
 DB 244 CTCTAATGCTTCTACCAAGCTGTTCCATAGAGATATTGTACAGGCGGATGACGTT 303
 QY 181 ATCTCTCACTTACCTGGCTGTGTCCTCGTGTAGCGCTTGGCAATCAATAACTCTG 240
 DB 304 ATTCTGACACACCCGCTGCAATCCTTGTCTCAGAGCGCAATATCACTCAGCTGTG 363
 QY 241 ATCCCTGTGAGCCCTTACCGCTGAGTCCGCTGCGCCGACCGCTCTCTCCG 300
 DB 364 ACCCGAGTGAACCTTACAGTGGAGTCAAGTACGTGGAGCAACCGCTTGAATACG 423
 QY 301 ACCGACGTGATATGATGTGGGAGGCGCAACCTTATGCTCAGCTCTTACGTAAGAGAC 360
 DB 424 AGTCATGTGACCTATTAGTGGCGCGCGCCACATGCTCTGCTCTTACGTGGTGA 483
 QY 361 CTGTGAGAGCGCTATTCTGTGAGGAGAGGGGTTCTCATGAGATGCCGCAATG 420
 DB 484 ATGTGTGGGGCTGTCTTCTCGTGGAGCAAGCCTTACGTTACAGACCTGTGCGCATCA 543
 QY 421 ACTGTCCAGACTGCAACTGTTT 443
 DB 544 ACGGTCCAGACCTGTAACTGCTC 566

RESULT 13
 ADP71119
 ID ADP71119 standard; cDNA; 630 BP.
 XX
 AC ADP71119;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE HCV DNA encoding E1 protein HCC162.
 XX
 KM Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KM liver disease; liver fibrosis; ss; serum alanine aminotransferase level;
 KM steatosis; anti-E2 immunoreactivity; vaccine.
 XX
 OS Hepatitis C virus; type 3a.
 XX
 PN US2004126395-A1.
 PD 01-JUL-2004.
 XX
 PF 18-DEC-2002; 2002US-00321798.
 XX
 PR 18-DEC-2001; 2001US-0453708P.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (MAER/) MAERTENS G.
 PA (DEPL/) DEPLA E.
 PA (BOSM/) BOSMAN F.
 PI Maertens G, Depla E, Bosman F;
 XX WPI; 2004-499089/47.
 DR P-PSDB; ADP71120.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
 PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
 XX immunoreactivity in the liver of a chronic HCV-infected mammal.
 PS Example 2; SEQ ID NO 29; 176pp; English.
 XX
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
 CC composition for reducing liver disease (such as liver fibrosis or its
 CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
 CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
 CC or for treating a chronic HCV-infected mammal. The liver disease is
 CC reduced by at least 1-2 points according to the overall Ishak score in
 CC the HCV-infected mammal. Also included are a method for predicting
 CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 CC HCV vaccine composition (comprising at least one purified or a
 CC combination of at least 2 HCV single or specific oligomeric recombinant
 CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 CC proteins, an E1/E2 protein complex formed from purified HCV single or
 CC specific oligomeric recombinant E1 or E2 proteins or its parts and
 CC optionally a pharmaceutical adjuvant), a composition (comprising at least
 CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
 CC immunogenic HCV composition (or HCV vaccine composition) comprising a
 CC recombinant virus allowing expression of at least one HCV recombinant
 CC envelope protein (selected from an E1 protein and/or an E2 protein, and
 CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 CC vaccine composition (comprising a recombinant virus allowing expression
 CC of at least one HCV recombinant envelope protein chosen from an E1
 CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 CC optionally, a pharmaceutical adjuvant). The HCV vaccine composition is
 CC useful for reducing liver disease (such as liver fibrosis or its
 CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
 CC infected mammal, particularly human. The HCV E1 proteins are useful for
 CC in vitro monitoring HCV disease or diagnosing the response to treatment
 CC of patients suffering from HCV infection. The present sequence is an HCV
 CC cDNA encoding an E1 protein (or fragment).

Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 12; Length 630;

Best Local Similarity 70.2%; Pred. No. 1.2e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

```
QY 1 GACGGAAATTAATTTCCCAACAGGGAATTTACCTGTTGCTTTCTATCTTCTTCTG 60
    |||||
DB 124 GACGGGATAAATTTGCAACAGGGAATTTGCCCCGTTGCTTTCTATTTTCTTCTC 183
QY 61 GCTTTGTTCTATGCTTCTTCAACCAACGCGGCTGAGTACCGTAATGCTCCGA 120
    |||||
DB 184 GCTTGTCTCTTCTTCAATTCACAGAGCTAGTGGGGAATACGTCGCG 243
QY 121 CTTCAATGATGTAATCAAGCTGCAAGTAAAGGTAATGATAGGCGCGGATAT 180
    |||||
DB 244 CTTATGTCCTTACCAACGCTGTTCCAAATGAGATGATGACAGGCGGATACGTT 303
QY 181 ATCTTCCACTTACCTGCTGTGTCCCTGCTACGCTTGGCAATACATCAAGATGCTG 240
    |||||
DB 304 ATTTGTCACACACCGGCTGCACTTGTGTCAAGAGGGAATACATCCAGTGTG 363
QY 241 ATTCCTGTGAGCCCTTACCGTCCGTAAGTCCGCTGCGCCGACCGCTCTCTCCG 300
    |||||
DB 364 ACCCCAGTACACCTACAGTGGCAGTCAAGTACGTGGAACACCGCTTCAATACG 423
QY 301 ACAGCAATGATATGATGAGGCGGCAACCTATGCTACGCTCTACGTAAGAGAC 360
    |||||
DB 424 AGTCAATGAGACCTATTAGTGGCGGCGCAAGATGCTGCGCTTACGTTGAGTAC 483
QY 361 CTTTGTGAGCGCTATTTCTTGTGAGGCAAGGTTTCTCATGAGATGCGCAGATG 420
    |||||
DB 484 ATGTGTGGGGCTGTCTTCTCGTGGGACAAGCTTACGTTACAGCTGTGCGCATCA 543
QY 421 ACTGTCCAGACTGCACTGTTTC 443
    |||||
DB 544 ACGGTCCAGACCTGTAACTGCTC 566
    |||||
```

RESULT 14

AA207658
ID AA207658 standard; DNA; 1249 BP.

XX AA207658;

XX 20-MAR-2003 (revised)

DT 08-NOV-1999 (first entry)

DE HCV J1 NS domain consensus DNA sequence.

XX Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;

KW HCV infection; vaccine; ds.

XX Hepatitis C virus.

OS

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PT New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
PT infections and development of vaccines.

XX Disclosure; Fig 14; 132pp; English.

XX The invention provides two new isolates of hepatitis C virus (HCV), J1
CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridization for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the NS1 domain consensus sequence of HCV
CC isolates J1 and HCV-1. (Updated on 20-MAR-2003 to correct PR field.)
CC (Updated on 20-MAR-2003 to correct PR field.)
XX

Sequence 1249 BP; 160 A; 282 C; 276 G; 206 T; 0 U; 325 Other;

Query Match 49.5%; Score 221.4; DB 2; Length 1249;

Best Local Similarity 54.6%; Pred. No. 7.2e-59;

Matches 244; Conservative 83; Mismatches 120; Indels 0; Gaps 0;

```
QY 1 GACGGAAATTAATTTCCCAACAGGGAATTTACCTGTTGCTTTCTATCTTCTTCTG 60
    |||||
DB 68 GACGGGATAAATTTGCAACAGGGAATTTGCCCCGTTGCTTTCTATTTTCTTCTC 127
QY 61 GCTTTGTTCTATGCTTCTTCAACCAACGCGGCTGAGTACCGTAATGCTCCGA 120
    |||||
DB 128 GCTTGTCTCTTCTTCAATTCACAGAGCTAGTGGGGAATACGTCGCG 187
QY 121 CTTCAATGATGTAATCAAGCTGCAAGTAAAGGTAATGATAGGCGCGGATAT 180
    |||||
DB 188 ATWTACCAATGATATGATGAGGCGGCAACCTATGCTACGCTCTACGTAAGAGAC 247
QY 181 ATCTTCCACTTACCTGCTGTGTCCCTGCTACGCTTGGCAATACATCAAGATGCTG 240
    |||||
DB 248 ATCTGTCACACACCGGCTGCACTTGTGTCAAGAGGGAATACATCCAGTGTG 307
QY 241 ATTCCTGTGAGCCCTTACCGTCCGTAAGTCCGCTGCGCCGACCGCTCTCTCCG 300
    |||||
DB 308 GTAGCGMTSACCCCTACAGTGGCGGCGCAAGATGCTGCGCTTACGTTGAGTAC 367
QY 301 ACAGCAATGATATGATGAGGCGGCAACCTATGCTACGCTCTACGTAAGAGAC 360
    |||||
DB 368 GCTGACRTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
QY 361 CTTTGTGAGCGCTATTTCTTGTGAGGCAAGGTTTCTCATGAGATGCGCAGATG 420
    |||||
DB 428 CTTTGTGAGCGCTATTTCTTGTGAGGCAAGGTTTCTCATGAGATGCGCAGATG 487
QY 421 ACTGTCCAGACTGCACTGTTTCATC 447
    |||||
DB 488 ACRRTYCARGRYTCGAAYTGTCTCATC 514
    |||||
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RESULT 15

AAQ35072
ID AAQ35072 standard; DNA; 565 BP.

XX AAQ35072;

XX 20-MAY-1993 (first entry)

DE HCV envelope region nucleic acid.

XX Envelope; region; type C; hepatitis; virus; HCV; vaccine; serum;

KW non-A, non-B; amplify; ss.

XX Hepatitis C virus.

OS

XX

XX

XX

XX

XX

XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: December 29, 2004, 14:44:07 ; Search time 75 Seconds

(Without alignments)
4236.302 Million cell updates/sec

Title: US-09-851-138c-51

Perfect score: 447
Sequence: 1 gacggaatcaatttcgcaac.....aggactcgaactgttcacac 447

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.8	99.7	447	3	US-08-836-075A-51
2	236.2	52.8	541	4	US-09-878-281A-13
3	236.2	52.8	541	4	US-09-878-281A-17
4	234.6	52.5	541	4	US-09-878-281A-19
5	233	52.1	541	4	US-09-878-281A-15
6	233	52.1	541	4	US-09-878-281A-21
7	233	52.1	541	4	US-09-878-281A-25
8	233	52.1	541	4	US-09-878-281A-27
9	233	52.1	630	3	US-08-612-973-29
10	233	52.1	630	3	US-08-612-973-29
11	231.4	51.8	541	4	US-09-878-281A-23
12	217.4	48.6	579	4	US-09-878-281A-177
13	215.8	48.3	579	4	US-09-878-281A-120
14	215.8	48.3	579	4	US-09-878-281A-175
15	215.8	48.3	579	4	US-09-878-281A-181
16	209.8	46.9	447	3	US-08-836-075A-39
17	209	46.8	447	3	US-08-836-075A-31
18	208.6	46.7	447	3	US-08-836-075A-37
19	206.6	46.2	579	4	US-09-878-281A-173
20	206.2	46.1	579	4	US-09-878-281A-187
21	205	45.9	579	4	US-09-878-281A-171
22	204.6	45.8	574	4	US-09-878-281A-118
23	204.2	45.7	2116	3	US-08-191-160-21
24	203	45.4	579	4	US-09-878-281A-155
25	201.4	45.1	579	4	US-09-878-281A-155
26	201.4	45.1	579	4	US-09-878-281A-155
27	201	45.0	447	3	US-08-836-075A-29

28	199.4	44.6	742	1	US-08-081-072-18	Sequence 18, App1
29	199.4	44.6	742	1	US-08-449-093A-18	Sequence 18, App1
30	199.4	44.6	932	1	US-08-081-072-15	Sequence 15, App1
31	199.4	44.6	932	1	US-08-449-093A-15	Sequence 15, App1
32	198.2	44.3	447	3	US-08-836-075A-35	Sequence 35, App1
33	197.8	44.3	447	3	US-08-836-075A-33	Sequence 33, App1
34	196.2	43.9	501	2	US-08-483-695-30	Sequence 30, App1
35	196.2	43.9	501	2	US-07-965-285-30	Sequence 30, App1
36	196.2	43.9	501	2	US-08-487-231-30	Sequence 30, App1
37	196.2	43.9	501	3	US-09-201-912-30	Sequence 30, App1
38	196.2	43.9	633	3	US-08-612-973-7	Sequence 7, App1
39	196.2	43.9	633	3	US-08-927-597-7	Sequence 7, App1
40	196.2	43.9	795	3	US-08-612-973-5	Sequence 5, App1
41	196.2	43.9	795	3	US-08-927-597-5	Sequence 5, App1
42	196.2	43.9	2082	3	US-08-612-973-47	Sequence 47, App1
43	196.2	43.9	2082	3	US-08-927-597-47	Sequence 47, App1
44	196.2	43.9	2433	3	US-08-612-973-49	Sequence 49, App1
45	196.2	43.9	2433	3	US-08-927-597-49	Sequence 49, App1

ALIGNMENTS

RESULT 1
US-08-836-075A-51

Sequence 51, Application US/08836075A

Patent No. 6180768

GENERAL INFORMATION:

APPLICANT: MAERTENS, GERT

APPLICANT: STUYVER, LIEVEN

TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC

NUMBER OF SEQUENCES: 207

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,075A

FILING DATE: 21 Apr 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/04155

FILING DATE: 23 Oct 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94870166.9

FILING DATE: 21 Oct 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95870076.7

FILING DATE: 28 Jun 1995

ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: INNS:004

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 447 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: linear

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-836-075A-51

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Query Match          99.7%; Score 445.8; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.7e-124;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACGGAATTAATTTCGCAACAGGAAATTTAAGCTGTTGCTCTTCTCTATCTTCTCTCTG 60
DB      1 GACGGAATTAATTTCGCAACAGGAAATTTAAGCTGTTGCTCTTCTCTATCTTCTCTCTG 60

QY      61 GCTTTGTTCTCATGCTTCTGCTTACACCCACAGCCGGGCTGAGTACCGTAAATGCTCCGA 120
DB      61 GCTTTGTTCTCATGCTTCTGCTTACACCCACAGCCGGGCTGAGTACCGTAAATGCTCCGA 120

QY      121 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 180
DB      121 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 180

QY      181 ATCTCTCACTTAAGTCTGCTGTGTGCTCCCTGAGTACGCTCTGGCAATACATCAAGATCTG 240
DB      181 ATCTCTCACTTAAGTCTGCTGTGTGCTCCCTGAGTACGCTCTGGCAATACATCAAGATCTG 240

QY      241 ATCCCTGTAGAGCCCTAACGCTCCGCTGGAAGTGGCCCTTGCGCCGACCGGCTCTCCGC 300
DB      241 ATCCCTGTAGAGCCCTAACGCTCCGCTGGAAGTGGCCCTTGCGCCGACCGGCTCTCCGC 300

QY      301 AGCAAGTGAATATGATGATGGGAGCGGCAACCTATGCTCAAGCTCTTACAGTAAAGAC 360
DB      301 AGCAAGTGAATATGATGATGGGAGCGGCAACCTATGCTCAAGCTCTTACAGTAAAGAC 360

QY      361 CTTTGTGAGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATAGAGATGCGCAGATGG 420
DB      361 CTTTGTGAGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATAGAGATGCGCAGATGG 420

QY      421 ACTGTCCAGACTGCAACTGTTCATC 447
DB      421 ACTGTCCAGACTGCAACTGTTCATC 447

RESULT 2
US-09-878-281A-13
; Sequence 13, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-13

Query Match          52.8%; Score 236.2; DB 4; Length 541;
Best Local Similarity 70.7%; Pred. No. 1.8e-61;
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

QY      1 GACGGAATTAATTTCGCAACAGGAAATTTAAGCTGTTGCTCTTCTCTATCTTCTCTCTG 60
DB      62 GACGGGATTAATTTCGCAACAGGAAATTTGCGGGTGTGCTCTTCTCTATCTTCTCTCTT 121

QY      61 GCTTTGTTCTCATGCTTCTGCTTACACCCACAGCCGGGCTGAGTACCGTAAATGCTCCGA 120
DB      122 GCTTTGTTCTCATGCTTCTGCTTACATCCAGAGCTAGTCTAGAGTGGGGAACAGTCTGGC 181

QY      121 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 180
DB      121 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 180

QY      181 ATCTCTCACTTAAGTCTGCTGTGTGCTCCCTGAGTACGCTCTGGCAATACATCAAGATCTG 240
DB      181 ATCTCTCACTTAAGTCTGCTGTGTGCTCCCTGAGTACGCTCTGGCAATACATCAAGATCTG 240
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DB      242 ATTCTGCACACACCCGGGCTGTGTACTTGTGTTACAGACGGTAATACATCTGCGTCTG 301

QY      241 ATCCCTGTAGAGCCCTAACGCTCCGCTGAAAGTGGCCCTTGCGCCGACCGGCTCTCTCCGC 300
DB      302 ACCCGAGTGAACACCTACAGTGGCAGTACAGTACGTACGTGAGGCAACACCGCTTCTGATCCG 361

QY      301 AGCAAGTGAATATGATGATGGGAGCGGCAACCTATGCTCAAGTCTCTACGTAAAGAC 360
DB      362 AGGCAATGTAATGATGATGGGAGCGGCAACCTATGCTCAAGTCTCTACGTAAAGAT 421

QY      361 CTTTGTGAGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATAGAGATGCGCAGATGG 420
DB      422 ATGTGTGGGCGGCTTCTCTCTGTGGGCAAGGCTTCAAGTTCAAGACTGTGCGCATCA 481

QY      421 ACTGTCCAGACTGCAACTGTTC 443
DB      482 ACTGTCCAGACTGCAACTGTTC 504

RESULT 3
US-09-878-281A-17
; Sequence 17, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-17

Query Match          52.8%; Score 236.2; DB 4; Length 541;
Best Local Similarity 70.7%; Pred. No. 1.8e-61;
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

QY      1 GACGGAATTAATTTCGCAACAGGAAATTTAAGCTGTTGCTCTTCTCTATCTTCTCTCTG 60
DB      62 GACGGGATTAATTTCGCAACAGGAAATTTGCGGGTGTGCTCTTCTCTATCTTCTCTCTT 121

QY      61 GCTTTGTTCTCATGCTTCTGCTTACACCCACAGCCGGGCTGAGTACCGTAAATGCTCCGA 120
DB      122 GCTTTGTTCTCATGCTTCTGCTTATCCATCCAGAGCTAGTAAAGTGGCGGAACAGTCTGGC 181

QY      121 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 180
DB      121 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 180

QY      181 ATCTCTCACTTAAGTCTGCTGTGTGCTCCCTGAGTACGCTCTGGCAATACATCAAGATCTG 240
DB      182 CTCTACATGTAATTAAGTACAGTCTGAGTAAAGGTAATGATGATGAGGCGGGGATATT 241

QY      181 ATCTCTCACTTAAGTCTGCTGTGTGCTCCCTGAGTACGCTCTGGCAATACATCAAGATCTG 240
DB      242 ATTTCTGCACACACCCGGGCTGTGTACTTGTGTGTTACAGACGGTAATACATCTGCGTCTG 301

QY      241 ATCCCTGTAGAGCCCTAACGCTCCGCTGAAAGTGGCCCTTGCGCCGACCGGCTCTCTCCGC 300
DB      302 ACCCGAGTGAACACCTACAGTGGCAGTCAAGTACGTCTGAGGCAACACCGCTTCTGATCCG 361

QY      301 AGCAAGTGAATATGATGATGGGAGCGGCAACCTATGCTCAAGTCTCTACGTAAAGAC 360
DB      362 AGGCAATGTAATGATGATGGGAGCGGCAACCTATGCTCAAGTCTCTACGTAAAGAT 421

QY      361 CTTTGTGAGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATAGAGATGCGCAGATGG 420
DB      422 ATGTGTGGGCGGCTTCTCTCTGTGGGCAAGGCTTCAAGTTCAAGACTGTGCGCATCA 481

QY      421 ACTGTCCAGACTGCAACTGTTC 443
```

Db 482 ACCGTCACAGCCTGTAACCTGCTC 504

RESULT 4

US-09-878-281A-19
Sequence 19, Application US/09878281A

Patent No. 6762024

GENERAL INFORMATION:

APPLICANT: Immunogenetics N.V.

TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph

FILE REFERENCE: 35

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 284

SOFTWARE: PatentIn version 3.1

SEQ ID NO 19

LENGTH: 541

TYPE: DNA

ORGANISM: hepatitis C virus

US-09-878-281A-19

Query Match 52.5%; Score 234.6; DB 4; Length 541;

Best Local Similarity 70.4%; Pred. No. 5,5e-61;

Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

1 GACGGAATTAATTTGGCAACAGGAAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60

62 GACGGGATTAATTTGGCAACAGGAAATTTGCGGTTGCTCTTCTCTATCTTCTCTG 121

61 GCTTTGTTCTCATGCTTGTCTTACACCAACGCGGGCTGGAATACCGTAATGCTCCGA 120

122 GCTGTTCTCTTCTTAACTTCAATCAGACAGTACGTAAGTGGGGAATACGTTGGC 181

121 CTCTACATGTAATTAACGACCTGACAGTACGTAAGTACGTAAGTACGCGGGAATAT 180

182 CTCTATGCTCTTACCAACAGCTGTTCCATAGACAGTATGTTGACAGGCGCATGACGTT 241

181 ATCTTCACCTTACCTGCTGTTGCTCCCTGCGTACGCTCTGGAATACATCAAGATCTGG 240

242 ATTCTGACACACCGCGGTGACATACCTTGTGTCAGAGACGGAATACATCACTGCTGG 301

241 ATCCCTGTGAGCCCTACCGTCCGCGGGAATGCGCCCTGCGCCGACCGCTCTCTCCG 300

302 ACCCGAGTACACCTTACAGTGCAGTCAAGTACGTGGAACCAACCGCTTGATACGC 361

301 ACCGACGTGATATGATGAGGCGGCGCACCTATGCTCAGCTCTCTACGTAAGAGAC 360

362 AGTCACTGTGACCTATTAGTGGCGCGGCGCACATGCTCAGCGCTCTACGTTGGAT 421

361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTGG 420

422 ATGTGTGGGCGCTCTTCTGTTGGGACAAGCCTTCACGTTACAGCTGTCGCATCA 481

421 ACTGTCCAGACATGCAACTGTTG 443

482 ACCGTCACAGCCTGTAACCTGCTC 504

RESULT 5

US-09-878-281A-15

Sequence 15, Application US/09878281A

Patent No. 6762024

GENERAL INFORMATION:

APPLICANT: Immunogenetics N.V.

TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph

FILE REFERENCE: 35

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 284

SOFTWARE: PatentIn version 3.1

LENGTH: 541

TYPE: DNA

ORGANISM: hepatitis C virus

US-09-878-281A-15

Query Match 52.1%; Score 233; DB 4; Length 541;

Best Local Similarity 70.2%; Pred. No. 1.7e-60;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

1 GACGGAATTAATTTGGCAACAGGAAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60

62 GACGGGATTAATTTGGCAACAGGAAATTTGCGGTTGCTCTTCTCTATCTTCTCTG 121

61 GCTTTGTTCTCATGCTTGTCTTACACCAACGCGGGCTGGAATACCGTAATGCTCCGA 120

122 GCTGTTCTCTTCTTAACTTCAATCAGACAGTACGTAAGTGGGGAATACGTTGGC 181

121 CTCTACATGTAATTAACGACCTGACAGTACGTAAGTACGTAAGTACGCGGGAATAT 180

182 CTCTATGCTCTTACCAACAGCTGTTCCATAGACAGTATGTTGACAGGCGCATACGTT 241

181 ATCTTCACCTTACCTGCTGTTGCTCCCTGCGTACGCTCTGGAATACATCAAGATCTGG 240

242 ATTCTGACACACCGCGGTGACATACCTTGTGTTACAGACGTAATACATCTGCGTCTG 301

241 ATCCCTGTGAGCCCTACCGTCCGCGGGAATGCGCCCTGCGCCGACCGCTCTCTCCG 300

302 ACCCGAGTACACCTTACAGTGCAGTCAAGTACGTGGAACCAACCGCTTGATACGC 361

301 ACCGACGTGATATGATGAGGCGGCGCACCTATGCTCAGCTCTCTACGTAAGAGAC 360

362 AGTCACTGTGACCTATTAGTGGCGCGGCGCACATGCTCTCTCTACGTTGGAT 421

361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTGG 420

422 ATGTGTGGGCGCTCTTCTGTTGGGACAAGCCTTCACGTTACAGCTGTCGCATCA 481

421 ACTGTCCAGACATGCAACTGTTG 443

482 ACCGTCACAGCCTGTAACCTGCTC 504

RESULT 6

US-09-878-281A-21

Sequence 21, Application US/09878281A

Patent No. 6762024

GENERAL INFORMATION:

APPLICANT: Immunogenetics N.V.

TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph

FILE REFERENCE: 35

CURRENT APPLICATION NUMBER: US/09/878,281A

CURRENT FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 284

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 541

TYPE: DNA

ORGANISM: hepatitis C virus

US-09-878-281A-21

Query Match 52.1%; Score 233; DB 4; Length 541;

Best Local Similarity 70.2%; Pred. No. 1.7e-60;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

1 GACGGAATTAATTTGGCAACAGGAAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60

62 GACGGGATTAATTTGGCAACAGGAAATTTGCGGTTGCTCTTCTCTATCTTCTCTG 121

61 GCTTTGTTCTCATGCTTGTCTTACACCAACGCGGGCTGGAATACCGTAATGCTCCGA 120

122 GCTGTTCTCTTCTTAACTTCAATCAGACAGTACGTAAGTGGGGAATACGTTGGC 181

[illegible]

```

RESULT 7
US-09-878-281A-25
; Sequence 25, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
; TITLE OF INVENTION: and therapy
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO 25
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-25

Query March 52.1%; Score 233; DB 4; Length 541;
Beet Local Similarity 70.2%; Pred. No. 1.7e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

Qy 1 GACGGAATTAATTCGCAACAGGGAATTAACCTGGTGCCTCTTCTATCTTCCTCTG 60
Db 62 GACGGGAATTAACCTGCAACAGGGGAATTTGCCGGTGTCTTTTCTATCTTCCTTCT 121

Qy 61 GCTTTGTTCTCATGCTGCTGCTTACACCAACGAGCCGGGCTGAGTACCGTAATGCTCCGGA 120
Db 122 GCTGTGTTCTTGTGTTATTCATTCATTCAGCACTGGTCTTAAGATGAGCGGAATACGTCGTGGC 181

Qy 121 CTTCACATGTAACCTAACAGACTGACAGTAAGGTATGATCGTATGAGGCGGGGAATATT 180
Db 182 CTCTATGCTCTTACCAACAGACTGTTCCATATGATATGATATGATAGAGCCGATGACGTT 241

Qy 181 ATCTCCACTTACCTGCTGTGTCCCTGCGCTACGCTCTGGCAATATACATCAAGATGCTGG 240
Db 242 ATTCTGACGCGCCCGGCTGTGTACTTGTGTCCAGAGCGGCATATAGTCTACATATGCTGG 301

Qy 241 ATCTCTGAGACCCCTACCGCTGCGCGTGAATGCGCCCTGCGCGCACCGCTCTCTCGC 300
Db 302 ACCCAAGTAACCTTACAGTGCAGTCAAGTACGTCCGGGGCAACACCGCTTCGATACGC 361

Qy 301 ACGCAGCGGATATGATGATGGGAGCGGCGCAACCCATGATCTCAGCTCTTACATGAGGAGAC 360
Db 362 AGTATATGAGACCTGTTATGATAGCGCGGCGCACGATGTCTTGGAGCTTTACGTGGATGAT 421

Qy 361 CTTGTGTGAGGCTAATTTCTTGTGTGGGAGGGGTTCTCATGAGAGACATCGCACATTTGG 420

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Db 422 ATGTGTGGGGCCGCTCTTCTCGTGGACAAGCTTCAAGTTCAGACCCCGCCGACATCAA 481

Qy 421 ACTGTCCAGGACGCAACGTTTC 443

Db 482 ACGGTCCAGACCTGTAACTGCTTC 504

```

RESULT 8
US-09-878-281A-27
; Sequence 27, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;
; LENGTH: 541
;
; TYPE: DNA
;
; ORGANISM: hepatitis C virus
US-09-878-281A-27

```

```

Query Match      52.1%; Score 233; DB 4; Length 541;
Best Local Similarity    70.2%; Pred. No. 1,7e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

Oy      1 GACGGAATTAATTTCGCAACAGGGAAATTTACCTGTGCTCTTCTCATCTTCCCTCG 60
        |||||
Db      62 GACGGGATAAAGCTTCGCAACAGGGAAATTTGCCGGTGCTCTTTTCTATCTTCCCTT 121

Oy      61 GCCTTGTCTCANGCTTGCCTTACACCACAAGCCGGGCTGAGTACCGTAAATGCTCCGA 120
        |||||
Db      122 GCTCTGTCTCTTCTTATTCATCCAGCAGCTGTGTATAGATGACGGAATACGTCTGC 181

Oy      121 CTTCACATNGTAATTAACGACTGCAATACGGTAAGTATCTGTATATGAGCCCGGGAAAT 180
        |||||
Db      182 CTTATATGCTCTTACCAACGACTGTTCATATAGTATGTATATGAGGCGGATGACGTT 241

Oy      181 ATCTCACACTTACCTGAGCTGTGTCCTCGGTACGCTCTGGAATATCATCAAGAATGCTG 240
        |||||
Db      242 ATTTCGACGCGCCCGGCTGTATCTTGTGTCCAGAACGGCAATATGCTTACATGCTGG 301

Oy      241 ATCCCTGTGAGCCCYAACCGTCCGCGTAGTGCGCCCTCGCCCGCACCGCTCTCTCCG 300
        |||||
Db      302 ACCCCAGTAACACCTTACAGTGCAGTACAGTACGTCCGGGGCAACACCGCTTCATAGC 361

Oy      301 ACGACCTGATATNGATGTGTGAGGCGGCCACCTTATGCTCAGTCTCTAAGTAGAGAC 360
        |||||
Db      362 AGTATATGTGACCTGTATGAGGCGGCCCAAGATGTGCTGTGCTTACGTGGGTGAT 421

Oy      361 CTTTGTGAGAGOGCTATTCTTGTGTGCGCAGGGGTCTCATAGSAGACATCCGACATYGG 420
        |||||
Db      422 ATGTGTGGGGCCGCTTCTCTGTGGGACAAAGCCTTACAGTTACAGCCCCCGGCATCAA 481

Oy      421 ACTGTCCAGACGTGCAACTGTTC 443
        |||||
Db      482 ACGSTCCAGACCTGTACTGCTC 504

RESULT 9
US-08-612-973-29
; Sequence 29, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSSE, MARIE-ANGE
```

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..624
NAME/KEY: mat peptide
LOCATION: 1..624
US-08-612-973-29

Query Match 52.1%; Score 233; DB 3; Length 630;
Best Local Similarity 70.2%; Pred. No. 1.8e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GAGGGAATTAATTGCGAAGGGAATTTACCTGCTTCTCTATCTTCTG 60
DB 124 GAGGGAATTAATTGCGAAGGGAATTTGCGGTTGCTCTTCTATTTCTTTC 183
QY 61 GCTTTGTTCTCATGCTTGTCTTAACCAAGCCGCGGCTGAGTACCGTAATGCTCCGA 120
DB 184 GCTCTGTTCTCTGCTTAATTCATCCAGGAGTACGTAAGTGGCGAATAGTCTGCG 243
QY 121 CTCTACATGTAATTAAGCACTGCAAGTACGTAAGTATGTAATGAGCGCGGGAATTT 180
DB 244 CTCTAGTCTCTTCAACGACGCTGTTCCATAGCAATGTAATGTAACGAGCGCATGAGTT 303
QY 181 ATGCTGCACTTACCTGCTGTGTCCCTGAGTACGCTGCGCAATCATCAAGATGCTGG 240
DB 304 ATTCTGACACACCGGCTGCATACCTTGTGTCAGAGCGCAATATACATCAGTGTGG 363
QY 241 ATCCCTGTGAGCCCAACCGTGCCTGAGTACGCTGCGCGCAACCGCTCTCTCCG 300
DB 364 ACCCAAGTACACCTACAGTGGCAGTCAAGTACGTAAGTGGCAACACCGCTTGGATACG 423
QY 301 ACCGAGTGTATATGATGTGGGCGCGCAACCTATGCTCAGTCTCTTACGTAAGAGAC 360
DB 424 AGTCATGTGACCTATTAAGTGGGCGCGCAACATGTGCTCTGCGCTTACGTAAGGAGTAC 483
QY 361 CTGTGAGAGCGGATTTCTGTGTGGGCAAGGGGTTCTCATGAGACATGCGACATGG 420

DB 484 ATGTGTGGGCGCTGTCTTCTCGTGGGCAAGGCTTACGTTACAGCTCGTGCATCA 543
QY 421 ACTGTCCAGACTGCACTGTTTC 443
DB 544 ACGGTCCAGACCTGTAACTGCTC 566

RESULT 10
US-08-927-597-29
Sequence 29, Application US/08927597
Patent No. 624503
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTINO, GUY
APPLICANT: BUYS, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..627
NAME/KEY: mat peptide
LOCATION: 1..624
US-08-927-597-29

Query Match 52.1%; Score 233; DB 3; Length 630;
Best Local Similarity 70.2%; Pred. No. 1.8e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GAGGGAATTAATTGCGAAGGGAATTTACCTGCTTCTCTATCTTCTG 60
DB 124 GAGGGAATTAATTGCGAAGGGAATTTGCGGTTGCTCTTCTATTTCTTTC 183
QY 61 GCTTTGTTCTCATGCTTGTCTTAACCAAGCCGCGGCTGAGTACCGTAATGCTCCGA 120
DB 184 GCTCTGTTCTCTGCTTAATTCATCCAGGAGTACGTAAGTGGCGAATAGTCTGCG 243

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QY 121 CTCATCATGATGTAACGACAGTGAACGAGTATGCTGATGAGCCGGGATATT 180
    |||||
Db 244 CTCATAGTCTTACCAACGACCTGTTCCAAATAGCAGATATGTGACAGGCCATGACGTT 303
QY 181 ATCTCTCACTTACCTGGCTGTGTCCCTCGGTAAGCTCTGGCAATACATCAAGATCTGG 240
    |||||
Db 304 ATCTGTCACACACCCCGCTGCAATCCTTGTGTCAAGACGGCAATATCATTCAGTCTGG 363
QY 241 ATCCCTGTAGAGCCGTAACCGTCCGCTGAAAGTGCCTGTGGCCGCGCACCGCTCTCCGCG 300
    |||||
Db 364 ACCCGCATACACTACAGTGCAGTCAAGTACGTGGAGCAACACCGCTTCGATACGC 423
QY 301 ACGCAGTGAATATGATGTGGGCGGCGGCAACCTTATGCTCAAGCTCTTACATGAGAGAC 360
    |||||
Db 424 AGTCATGTGACCTATTAGTGGGCGGCGGCAAGATGTGCTGCGCTTACAGTGGGTGAC 483
QY 361 CTTTGTGAGGCGCTATTTCTTGTGGGCGAGGGTTCTCATGAGACATGCGCAGCATTTGG 420
    |||||
Db 484 ATGTGTGGGGCTGTCTTCTCGGGGCAAGCCTTCACGTCAGACCTGTGCGCATCA 543
QY 421 ACTGTCCAGACTGCACTGTTTC 443
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Db 544 ACGGTCCAGACTGTACTGCTC 566
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RESULT 11
US-09-878-281A-23
; Sequence 23, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Imogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-23
```

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Query Match 51.8%; Score 231.4; DB 4; Length 541;
Best Local Similarity 70.0%; Pred. No. 5,1e-60;
Matches 310; Conservative 1; Mismatches 132; Indels 0; Gaps 0;
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QY 1 GACGGAATTAATTTGGCAACAGGAAATTTACCTGTGCTCTTCTCTATCTTCTCTTG 60
    |||||
Db 62 GACGGGATTAACCTTGGCAACAGGAAATTTGCCGGTGTCTCTTCTATCTTCTCTTG 121
QY 61 GCTTTGTTCTCATGCTGCTTACACCCACAGCCGGCTGAGTACCGTATGCTCCGGA 120
    |||||
Db 122 GCTGTGTTCTCTTATTCATCCAGAGCTGTGCTAGAGTGGGGGAATACGTCTGAC 181
QY 121 CTCATCATGATGTAACGACAGTGAACGGAATGATGATGATGAGGCGGGGATATT 180
    |||||
Db 182 CTCATATGCTTACCAACGACAGTGTTCATATGATGATGATGAGGCGGATGACGTT 241
QY 181 ATCTCTCACTTACCTGGCTGTGTCCCTGCGTAAGCTCTGGCAATACATCAAGATGCTGG 240
    |||||
Db 242 ATCTGTCACAGCCGCGGCTGTGTACCTTGTGTCCAGACGGGCAATACGTCTACATGCTGG 301
QY 241 ATCCCTGTAGAGCCCTAACCGTCCGCGTGAAGTGCCTGTGGCCGCCACCGCTCTCTCCGC 300
    |||||
Db 302 ACCCGCATACACTACAGTGCAGTCAAGTACGTCGCGGCAACACCGCTTCGATACGC 361
QY 301 ACGCAGTGAATATGATGTGGGCGGCGGCAACCTTATGCTCAAGCTCTTACAGTGAAGAC 360
    |||||
Db 362 AGTCATGTGACCTGTATGATGAGGCGGCGGCAAGATGTGCTTACGCTTATGAGTGTAT 421
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QY 361 CTTTGTGAGCGCTATTTCTTGTGGGAGGGGTTCTCATGAGACATGCCAGCATTTGG 420
    |||||
Db 422 ATGTGTGGGGCGGTCTTCTCTGTGGGACAAAGCTTCAAGTTCAAGACCCGGCCATCA 481
QY 421 ACTGTCCAGACTGCACTGTTTC 443
    |||||
Db 482 ACGGTCCAGACTGTACTGCTC 504
    |||||
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```
RESULT 12
US-09-878-281A-177
; Sequence 177, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Imogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
; LENGTH: 579
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-177
```

```
Query Match 48.6%; Score 217.4; DB 4; Length 579;
Best Local Similarity 67.6%; Pred. No. 8,4e-56;
Matches 302; Conservative 2; Mismatches 143; Indels 0; Gaps 0;
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QY 1 GACGGAATTAATTTGGCAACAGGAAATTTACCTGTGCTCTTCTCTATCTTCTCTTG 60
    |||||
Db 100 GACGGGATTAACCTTGGCAACAGGAAATTTGCCGGTGTCTCTTCTATCTTCTCTTG 159
QY 61 GCTTTGTTCTCATGCTGCTTACACCCACAGCCGGCTGAGTACCGTATGCTCCGGA 120
    |||||
Db 160 GTCATTTCTCTGCGGCTTAACGTGTCCAGAGTGTGCTGCAAGACCGGAATGATCGGGC 219
QY 121 CTCATCATGATGTAACGACAGTGAACGGAATGATGATGATGAGGCGGGGATATT 180
    |||||
Db 220 ATCTACATGTCACCAAGACAGTCCGGAATTCATATGATGATGAGGCGGACATCAAC 279
QY 181 ATCTCTCACTTACCTGGCTGTGTCCCTGCGTAAGCTCTGGCAATACATCAAGATGCTGG 240
    |||||
Db 280 ATCATGACACTACCCGGGTGTGTGCTGTGTGAAGATGCTGCGGTGCTGG 339
QY 241 ATCCCTGTAGAGCCGTAACCGTCCGCTGGAAGTGCCTGTGGCCGCCACCGCTCTCTCCGC 300
    |||||
Db 340 ATCTCTTAAACACCCAGTGAAGCGTCCCTTACCTCGGGGCTCCATTAAGTGTGACGG 399
QY 301 ACGCAGTGAATATGATGTGGGCGGCGGCAACCTTATGCTCAAGCTCTTACATGAGAGAC 360
    |||||
Db 400 CAGCATGTGACCTGATGTGTGGGCGGCGGCAACCTTATGCTGCTCTTACATGAGAGAC 459
QY 361 CTTTGTGAGGCGCTATTTCTTGTGGGCGAGGGTTCTCATGAGACATGCGCAGCATTTGG 420
    |||||
Db 460 CATTTGCGAGGTGTCTTCTTGGCAGGCGAGATGTGCAATTTCCAAACCCGGGTATTTGG 519
QY 421 ACTGTCCAGACTGCACTGTTTCATC 447
    |||||
Db 520 ACTACCCAGATGCACTGTTTCATC 546
    |||||
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```
RESULT 13
US-09-878-281A-120
; Sequence 120, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Imogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
```

FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 120
LENGTH: 574
TYPE: DNA
ORGANISM: hepatitis C virus
US-09-878-281A-120

Query Match 48.3%; Score 215.8; DB 4; Length 574;
Best Local Similarity 67.3%; Pred. No. 2.5e-55;
Matches 301; Conservative 2; Mismatches 144; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTACCTGTTGCTCTTCTATCTTCTCTG 60
DB 100 GACGGGATTAATCATCAACAGGGAATCTTCCGGTGTCTCTTCTATCTTCTCTA 159
QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCCGGGCTGAGTACCGTATGCTCCGA 120
DB 160 GCACTTCTCTCGTGTGCTTGACTGTCCGGCTCGGCGGACATCACTTCGGGC 219
QY 121 CTCTACATGTAATTAACAGACTGCAAGTACGTAATGCTATGAGCGCGGATATT 180
DB 220 ATTATACAGTACCAATAGTACCTCCGGAATCTAGTATGATGAGTGAACATCAT 279
QY 181 ATCTCCACTTACCTGCTGTGTCCCTGTGAGTACGCTCTGGAATACATCAAGATGCTG 240
DB 280 ATCATGATCTACCAAGGATGTGTGCTGTGAGAAACCGGAAACACTCGCTGCTGG 339
QY 241 ATCCCTGTAGCCCTAACCTGCGCGGTGAAATGCGCCCTGCGCCGCTCTCTCCG 300
DB 340 GTTCTCTTAACACCACTGTGCTGCTCCCTATGTTGGCGCGCTCGAATCATGCGG 399
QY 301 ACGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 400 CGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 459
QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGATTTCTCATGAGACATCGCAGATTGG 420
DB 460 CTTTGTGAGGATGTCTTCTGTGTGGGCAAGATTTCATCTTCCGGCGCGCGCATTTGG 519
QY 421 ACTGTCCAGACTGCACTGTTCATC 447
DB 520 ACTACCCAGACTGCAACTGTCTTATC 546

RESULT 14

US-09-878-281A-175
Sequence 175, Application US/09878281A
Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 175
LENGTH: 579
TYPE: DNA
ORGANISM: hepatitis C virus
US-09-878-281A-175

Query Match 48.3%; Score 215.8; DB 4; Length 579;
Best Local Similarity 67.3%; Pred. No. 2.5e-55;
Matches 301; Conservative 2; Mismatches 144; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTACCTGTTGCTCTTCTATCTTCTCTG 60
DB 100 GACGGGATTAATCATCAACAGGGAATCTTCCGGTGTCTCTTCTATCTTCTCTA 159
QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCCGGGCTGAGTACCGTATGCTCCGA 120
DB 160 GCACTTCTCTCGTGTGCTTGAATGTCCGGCTCGGCGGACATCACTTCGGGC 219
QY 121 CTCTACATGTAATTAACAGACTGCAAGTACGTAATGCTATGAGCGCGGATATT 180
DB 220 ATTATACAGTACCAATAGTACCTCCGGAATCTAGTATGATGAGTGAACATCAT 279
QY 181 ATCTCCACTTACCTGCTGTGTCCCTGTGAGTACGCTCTGGAATACATCAAGATGCTG 240
DB 280 ATCATGATCTACCAAGGATGTGTGCTGTGAGAAACCGGAAACACTCGCTGCTGG 339

DB 100 GACGGGATTAATCATCAACAGGGAATCTTCCGGTGTCTCTTCTATCTTCTCTA 159
QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCCGGGCTGAGTACCGTATGCTCCGA 120
DB 160 GCACTTCTCTCGTGTGCTTGAATGTCCGGCTCGGCGGACATCACTTCGGGC 219
QY 121 CTCTACATGTAATTAACAGACTGCAAGTACGTAATGCTATGAGCGCGGATATT 180
DB 220 ATTATACAGTACCAATAGTACCTCCGGAATCTAGTATGATGAGTGAACATCAT 279
QY 181 ATCTCCACTTACCTGCTGTGTCCCTGTGAGTACGCTCTGGAATACATCAAGATGCTG 240
DB 280 ATCATGATCTACCAAGGATGTGTGCTGTGAGAAACCGGAAACACTCGCTGCTGG 339
QY 241 ATCCCTGTAGCCCTAACCTGCGCGGTGAAATGCGCCCTGCGCCGCTCTCTCCG 300
DB 340 GTTCTCTTAACACCACTGTGCTGCTCCCTATGTTGGCGCGCTCGAATCATGCGG 399
QY 301 ACGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 400 CGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 459
QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGATTTCTCATGAGACATCGCAGATTGG 420
DB 460 CTTTGTGAGGATGTCTTCTGTGTGGGCAAGATTTCATCTTCCGGCGCGCGCATTTGG 519
QY 421 ACTGTCCAGACTGCACTGTTCATC 447
DB 520 ACTACCCAGACTGCAACTGTCTTATC 546

RESULT 15

US-09-878-281A-181
Sequence 181, Application US/09878281A
Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 181
LENGTH: 579
TYPE: DNA
ORGANISM: hepatitis C virus
FEATURE:
NAME/KEY: misc feature
LOCATION: (152)..(152)
OTHER INFORMATION: "n" is any nucleotide
US-09-878-281A-181

Query Match 48.3%; Score 215.8; DB 4; Length 579;
Best Local Similarity 67.5%; Pred. No. 2.5e-55;
Matches 301; Conservative 1; Mismatches 144; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTACCTGTTGCTCTTCTATCTTCTCTG 60
DB 100 GACGGGATTAATCATCAACAGGGAATCTTCCGGTGTCTCTTCTATCTTCTCTA 159
QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCCGGGCTGAGTACCGTATGCTCCGA 120
DB 160 GCACTTCTCTCGTGTGCTTGAATGTCCGGCTCGGCGGACATCACTTCGGGC 219
QY 121 CTCTACATGTAATTAACAGACTGCAAGTACGTAATGCTATGAGCGCGGATATT 180
DB 220 ATTATACAGTACCAATAGTACCTCCGGAATCTAGTATGATGAGTGAACATCAT 279
QY 181 ATCTCCACTTACCTGCTGTGTCCCTGTGAGTACGCTCTGGAATACATCAAGATGCTG 240
DB 280 ATCATGATCTACCAAGGATGTGTGCTGTGAGAAACCGGAAACACTCGCTGCTGG 339

QY	241	ATCCCTGAGAGCCCTYACCCGTCGCCCGGTAAGTCGGCCTCGGGCCGACACGGCTCTCTCCG	300
Db	340	GTATCTCTGACACCTTACTGTGGCTGTCTCCCTACCTGGGGGCTCCGCTTACGTGCTAACGG	399
QY	301	ACGCACGTGGATATGATGTGTGGGRRGGGACACCCCTATNGCTCAGCTCTTACGTAGAGAG	360
Db	400	CGGCATGTGGATTTTGAATGTGGGTGACAGCACCCCTTGTCTCCCTCTACGTGGAGAC	459
QY	361	CTTTGTGAGCGCCTATTTCTTGTGTTGGGACGGGGTTCTCATNGAGACATCGCCAGATTGG	420
Db	460	CTCTGTGAGGGTGTCTTCTTCAAGGAGACAGATGTTCACCTTCAGCGCGGCCGCACTGG	519
QY	421	ACTGTCCAGGACTGCACACTGTTCCAT	446
Db	520	ACCACCTCAGAGCTGCACACTGTTCCAT	545

Search completed: December 29, 2004, 16:01:13
Job time : 82 secs